

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	1277	100.0	251	1	US-08-425-336-101	Sequence 101, App	
2	1277	100.0	251	1	US-08-488-113B-101	Sequence 101, App	
3	1277	100.0	251	1	US-08-477-484B-101	Sequence 101, App	
4	1277	100.0	251	1	US-08-646-360-101	Sequence 101, App	
5	1277	100.0	251	2	US-08-839-765-101	Sequence 101, App	
6	1277	100.0	251	2	US-09-136-389-101	Sequence 101, App	
7	1277	100.0	251	2	US-09-610-838-101	Sequence 101, App	
8	1277	100.0	251	2	US-09-711-485-101	Sequence 101, App	
9	1273	99.7	251	1	US-08-425-336-99	Sequence 99, Appl	
10	1273	99.7	251	1	US-08-425-336-100	Sequence 100, App	
11	1273	99.7	251	1	US-08-488-113B-99	Sequence 99, Appl	
12	1273	99.7	251	1	US-08-488-113B-100	Sequence 100, App	
13	1273	99.7	251	1	US-08-477-484B-99	Sequence 99, Appl	
14	1273	99.7	251	1	US-08-477-484B-100	Sequence 100, App	
15	1273	99.7	251	1	US-08-646-360-99	Sequence 99, Appl	
16	1273	99.7	251	1	US-08-646-360-100	Sequence 100, App	
17	1273	99.7	251	2	US-08-839-765-99	Sequence 99, Appl	
18	1273	99.7	251	2	US-08-839-765-100	Sequence 100, App	
19	1273	99.7	251	2	US-09-136-389-99	Sequence 99, Appl	
20	1273	99.7	251	2	US-09-136-389-100	Sequence 100, App	
21	1273	99.7	251	2	US-09-610-838-99	Sequence 99, Appl	
22	1273	99.7	251	2	US-09-610-838-100	Sequence 100, App	
23	1273	99.7	251	2	US-09-711-485-99	Sequence 99, Appl	
24	1273	99.7	251	2	US-09-711-485-100	Sequence 100, App	
25	1269	99.4	251	1	US-08-425-336-2	Sequence 2, Appl	
26	1269	99.4	251	1	US-08-425-336-110	Sequence 110, App	
27	1269	99.4	251	1	US-08-488-113B-2	Sequence 2, Appl	

Query Match 100.0%; Score 1277; DB 1; Length 251;
Best Local Similarity 100.0%; Pred. No. 9.8e-119; Indels 0; Gaps 0;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 GLDVSFSTKGATITVYVNFNLRLVKLPKGNHSHGIPLLRKKADDPGKAFVLVALSNDN 60
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DB 121 AYRETTDLGIEPLRIGIKLDENADNPKTEIASLLVWVQVSEARFTFIENQIRNN 180
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DB 181 FQQRIRPANNNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
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RESULT 2

US-08-488-113B-101
; Sequence 101, Application US/08488113B
; Patent No. 5744580
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,113B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 101:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-488-113B-101
Query Match 100.0%; Score 1277; DB 1; Length 251;
Best Local Similarity 100.0%; Pred. No. 9.8e-119; Indels 0; Gaps 0;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 GLDVSFSTKGATITVYVNFNLRLVKLPKGNHSHGIPLLRKKADDPGKAFVLVALSNDN 60
QY 61 GOLAEIAIDVTSVYVWGQVNRNSYFFKDAADAAAYEGLFKNTIKTRLHFGSGYSLEGEK 120
DB 61 GOLAEIAIDVTSVYVWGQVNRNSYFFKDAADAAAYEGLFKNTIKTRLHFGSGYSLEGEK 120
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DB 121 AYRETTDLGIEPLRIGIKLDENADNPKTEIASLLVWVQVSEARFTFIENQIRNN 180
QY 181 FQQRIRPANNNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
DB 181 FQQRIRPANNNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251
RESULT 3
US-08-477-484B-101
; Sequence 101, Application US/08477484B
; Patent No. 5756699
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
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; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
TELEPHONE: 312/707-9155
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-477-484B-101

Query Match 100.0%; Score 1277; DB 1; Length 251;
Best Local Similarity 100.0%; Pred. No. 9.8e-119;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GLDVSFSTKGATITVYVFNELRVKLPKGNHGIPLLRKADDPGKAPVLVALSNDN 60
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Db 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKADPAAYEGLFKNTIKTRLHFGGSYPSLSEK 120
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Db 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTETIASLLVVIQWSEAAARFTFIENQIRNN 180
Qy 181 FQORIRPANNTISLENKWKLSFOIRTSGANGMFSEAVELERANGKYYVTVAVDQVRPKI 240
Db 181 FQORIRPANNTISLENKWKLSFOIRTSGANGMFSEAVELERANGKYYVTVAVDQVRPKI 240
Qy 241 ALLKFVDKDPK 251
Db 241 ALLKFVDKDPK 251

RESULT 4
US-08-646-360-101
Sequence 101, Application US/08646360
Patent No. 5837491
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen P.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELEPHONE: 312/707-9155
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-646-360-101

Query Match 100.0%; Score 1277; DB 1; Length 251;
Best Local Similarity 100.0%; Pred. No. 9.8e-119;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GLDVSFSTKGATITVYVFNELRVKLPKGNHGIPLLRKADDPGKAPVLVALSNDN 60
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Db 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTETIASLLVVIQWSEAAARFTFIENQIRNN 180
Qy 181 FQORIRPANNTISLENKWKLSFOIRTSGANGMFSEAVELERANGKYYVTVAVDQVRPKI 240
Db 181 FQORIRPANNTISLENKWKLSFOIRTSGANGMFSEAVELERANGKYYVTVAVDQVRPKI 240
Qy 241 ALLKFVDKDPK 251
Db 241 ALLKFVDKDPK 251

RESULT 5
US-08-639-765-101
Sequence 101, Application US/08839765
Patent No. 6146631
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen P.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA


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; ZIP: 60661
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; SOFTWARE: Patent In Release #1.0, Version #1.25
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; FILING DATE: 15-APR-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
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; FILING DATE: 09-DEC-1992
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; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 101:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-839-765-101

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Best Local Similarity 100.0%; Pred. No. 9.8e-119; Indels 0; Gaps 0;
Matches 251; Conservative 0; Mismatches 0;

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Db 1 GLDVSFSTKGATITVYVFNELRVKLPKGNHGIPLLRKADDPGKAFVLVALSNDN 60

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Db 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTETIASLLVVIQWSEARFTFIENQIRNN 180

Qy 181 FQQRIRPANNTISLENKWKLSFOIRTSANGMPSEAVELERANGKKYVYVAVDQVKPKI 240
Db 181 FQQRIRPANNTISLENKWKLSFOIRTSANGMPSEAVELERANGKKYVYVAVDQVKPKI 240

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; APPLICATION NUMBER: US/08/839,765
; FILING DATE: 15-APR-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
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; APPLICATION NUMBER: US 08/064,691
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; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 101:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-839-765-101

Query Match 100.0%; Score 1277; DB 2; Length 251;
Best Local Similarity 100.0%; Pred. No. 9.8e-119; Indels 0; Gaps 0;
Matches 251; Conservative 0; Mismatches 0;

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; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/839,765
; FILING DATE: 15-APR-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
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; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 101:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-839-765-101

Query Match 100.0%; Score 1277; DB 2; Length 251;
Best Local Similarity 100.0%; Pred. No. 9.8e-119; Indels 0; Gaps 0;
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/136,389
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 101:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-136-389-101

Query Match 100.0%; Score 1277; DB 2; Length 251;
Best Local Similarity 100.0%; Pred. No. 9.8e-119; Indels 0; Gaps 0;
Matches 251; Conservative 0; Mismatches 0;

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Db 1 GLDVSFSTKGATITVYVFNELRVKLPKGNHGIPLLRKADDPGKAFVLVALSNDN 60

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RESULT 6

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US-09-136-389-101
; Sequence 101, Application US/09136389
; Patent No. 6146850
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
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Qy 241 ALLKFDKDPK 251
Db 241 ALLKFDKDPK 251

RESULT 7
US-09-610-838-101
; Sequence 101, Application US/09610838
; Patent No. 6376217
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/610,838
; FILING DATE: 06-JUL-2000
; CLASSIFICATION:
; APPLICATION NUMBER: US/09/136,389
; FILING DATE: 18-AUG-1998
; APPLICATION NUMBER: 08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 101:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-610-838-101

Query Match 100.0%; Score 1277; DB 2; Length 251;
Best Local Similarity 100.0%; Pred. No. 9.8e-119;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLDTVSFSTKGATYITVNFNLRVKLKPEGNSHGIPLLRKKADDPGKAPVLVALSNDN 60
Db 61 GQLAEIAIDVTSVVVVGQVVRNRSYFFKADAPDAAYEGLFKNTIKTRLHFGSGYPSLEGEK 120
61 GQLAEIAIDVTSVVVVGQVVRNRSYFFKADAPDAAYEGLFKNTIKTRLHFGSGYPSLEGEK 120
Qy 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTETAIASSLLVVIQWVSEAAARPTFIENQIRNN 180
Db 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTETAIASSLLVVIQWVSEAAARPTFIENQIRNN 180
Qy 181 FOQIRPANNITISLENKWKGLSFOIRTSYGANGMFSEAVELERANGKYYVTVAVDQVVKPKI 240
Db 181 FOQIRPANNITISLENKWKGLSFOIRTSYGANGMFSEAVELERANGKYYVTVAVDQVVKPKI 240
Qy 241 ALLKFDKDPK 251
Db 241 ALLKFDKDPK 251

RESULT 8
US-09-711-485-101
; Sequence 101, Application US/09711485
; Patent No. 6649742
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/711,485
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/839,765
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 101:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid


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;
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-711-485-101

Query Match      100.0%; Score 1277; DB 2; Length 251;
Best Local Similarity 100.0%; Pred. No. 9.8e-119;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLDVSFSTKGATITTYVNFNLRLVKLPKGNHSHGIPLLRKKADDPGKAPVLVALSNDN 60
Db 1 GLDVSFSTKGATITTYVNFNLRLVKLPKGNHSHGIPLLRKKADDPGKAPVLVALSNDN 60

Qy 61 GOLAEIAIDVTSVYVVGQVNRNSYFFKDAADAAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
Db 61 GOLAEIAIDVTSVYVVGQVNRNSYFFKDAADAAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120

Qy 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQWVSEAAARFTFIENQIRNN 180
Db 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQWVSEAAARFTFIENQIRNN 180

Qy 181 FQQRIRPANNITISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
Db 181 FQQRIRPANNITISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240

Qy 241 ALLKFVDKDPK 251
Db 241 ALLKFVDKDPK 251

RESULT 9
US-08-425-336-99
; Sequence 99, Application US/08425336
; Patent No. 5621083
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425,336
; FILING DATE: 18-APR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Thomas C.
; REGISTRATION NUMBER: P-36,989
; REFERENCE/DOCKET NUMBER: 31394
; TELEPHONE: 312/474-0448
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 99:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-425-336-99

Query Match      99.7%; Score 1273; DB 1; Length 251;
Best Local Similarity 99.6%; Pred. No. 2.5e-118;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLDVSFSTKGATITTYVNFNLRLVKLPKGNHSHGIPLLRKKADDPGKAPVLVALSNDN 60
Db 1 GLDVSFSTKGATITTYVNFNLRLVKLPKGNHSHGIPLLRKKADDPGKAPVLVALSNDN 60

Qy 61 GOLAEIAIDVTSVYVVGQVNRNSYFFKDAADAAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
Db 61 GOLAEIAIDVTSVYVVGQVNRNSYFFKDAADAAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120

Qy 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQWVSEAAARFTFIENQIRNN 180
Db 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQWVSEAAARFTFIENQIRNN 180

Qy 181 FQQRIRPANNITISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
Db 181 FQQRIRPANNITISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240

Qy 241 ALLKFVDKDPK 251
Db 241 ALLKFVDKDPK 251

RESULT 10
US-08-425-336-100
; Sequence 100, Application US/08425336
; Patent No. 5621083
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425,336
; FILING DATE: 18-APR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Thomas C.
; REGISTRATION NUMBER: P-36,989
; REFERENCE/DOCKET NUMBER: 31394
; TELEPHONE: 312/474-0448
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 99:
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TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-425-336-100

Query Match 99.7%; Score 1273; DB 1; Length 251;
Best Local Similarity 99.6%; Pred. No. 2.5e-118;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLDTSFSTKGATITYYVNFNLRLVKLPKGNHSHGIPLLRKKADDPKAFVLVNSNDN 60
Db 1 GLDTSFSTKGATITYYVNFNLRLVKLPKGNHSHGIPLLRKKADDPKAFVLVNSNDN 60
Qy 61 GOLAEIAIDVTSVVGQVNRNSYFFPKADPAAYEGLFKNTIKTRLHFGSGYPSLGEK 120
Db 61 GOLAEIAIDVTSVVGQVNRNSYFFPKADPAAYEGLFKNTIKTRLHFGSGYPSLGEK 120
Qy 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTETIASLLVVIQWYSEAAFTFIENQIRNN 180
Db 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTETIASLLVVIQWYSEAAFTFIENQIRNN 180
Qy 181 FQQRIRPANNITISLENKWKLSFQIRTSANGMFPSEAVELERANGKYYVTVAVDQVKPKI 240
Db 181 FQQRIRPANNITISLENKWKLSFQIRTSANGMFPSEAVELERANGKYYVTVAVDQVKPKI 240
Qy 241 ALLKFVDKDPK 251
Db 241 ALLKFVDKDPK 251

RESULT 11

US-08-488-113B-99
Sequence 99, Application US/08488113B
Patent No. 5744580
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,113B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707

FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/200-70.F3.C2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-488-113B-99

Query Match 99.7%; Score 1273; DB 1; Length 251;
Best Local Similarity 99.6%; Pred. No. 2.5e-118;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLDTSFSTKGATITYYVNFNLRLVKLPKGNHSHGIPLLRKKADDPKAFVLVNSNDN 60
Db 1 GLDTSFSTKGATITYYVNFNLRLVKLPKGNHSHGIPLLRKKADDPKAFVLVNSNDN 60
Qy 61 GOLAEIAIDVTSVVGQVNRNSYFFPKADPAAYEGLFKNTIKTRLHFGSGYPSLGEK 120
Db 61 GOLAEIAIDVTSVVGQVNRNSYFFPKADPAAYEGLFKNTIKTRLHFGSGYPSLGEK 120
Qy 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTETIASLLVVIQWYSEAAFTFIENQIRNN 180
Db 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTETIASLLVVIQWYSEAAFTFIENQIRNN 180
Qy 181 FQQRIRPANNITISLENKWKLSFQIRTSANGMFPSEAVELERANGKYYVTVAVDQVKPKI 240
Db 181 FQQRIRPANNITISLENKWKLSFQIRTSANGMFPSEAVELERANGKYYVTVAVDQVKPKI 240
Qy 241 ALLKFVDKDPK 251
Db 241 ALLKFVDKDPK 251

RESULT 12
US-08-488-113B-100
Sequence 100, Application US/08488113B
Patent No. 5744580
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,113B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:


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; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-488-113B-100

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Query Match          99.7%; Score 1273; DB 1; Length 251;
Best Local Similarity 99.6%; Pred. No. 2.5e-118;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLDVSFSTKGATITVYVNFNLRLVKLPKGNHSHGIPLLRKADDPGKAFVLVSLNDN 60
Db 1 GLDVSFSTKGATITVYVNFNLRLVKLPKGNHSHGIPLLRKADDPGKAFVLVSLNDN 60

Qy 61 GOLAEIAIDVTSVYVVGQVNRNSYFFPKDAPDAAYEGLFKNTIKTRLHFGGSYPSLSEGEK 120
Db 61 GOLAEIAIDVTSVYVVGQVNRNSYFFPKDAPDAAYEGLFKNTIKTRLHFGGSYPSLSEGEK 120

Qy 121 AYRETTDLGIEPLRIGIKKLDENADINYPKTEIASLLVLIQWVSEAAARFTFIENQIRNN 180
Db 121 AYRETTDLGIEPLRIGIKKLDENADINYPKTEIASLLVLIQWVSEAAARFTFIENQIRNN 180

Qy 181 FQQRIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240
Db 181 FQQRIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240

Qy 241 ALLKFDVKDPK 251
Db 241 ALLKFDVKDPK 251

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RESULT 13
US-08-477-484B-99
; Sequence 99, Application US/08477484B
; Patent No. 5756699
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,484B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-9155
; TELEFAX: 312/707-8889
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 99:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-477-484B-99

Query Match          99.7%; Score 1273; DB 1; Length 251;
Best Local Similarity 99.6%; Pred. No. 2.5e-118;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLDVSFSTKGATITVYVNFNLRLVKLPKGNHSHGIPLLRKADDPGKAFVLVSLNDN 60
Db 1 GLDVSFSTKGATITVYVNFNLRLVKLPKGNHSHGIPLLRKADDPGKAFVLVSLNDN 60

Qy 61 GOLAEIAIDVTSVYVVGQVNRNSYFFPKDAPDAAYEGLFKNTIKTRLHFGGSYPSLSEGEK 120
Db 61 GOLAEIAIDVTSVYVVGQVNRNSYFFPKDAPDAAYEGLFKNTIKTRLHFGGSYPSLSEGEK 120

Qy 121 AYRETTDLGIEPLRIGIKKLDENADINYPKTEIASLLVLIQWVSEAAARFTFIENQIRNN 180
Db 121 AYRETTDLGIEPLRIGIKKLDENADINYPKTEIASLLVLIQWVSEAAARFTFIENQIRNN 180

Qy 181 FQQRIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240
Db 181 FQQRIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240

Qy 241 ALLKFDVKDPK 251
Db 241 ALLKFDVKDPK 251

RESULT 14
US-08-477-484B-100
; Sequence 100, Application US/08477484B
; Patent No. 5756699
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.

```


;; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;; TITLE OF INVENTION: Proteins
;; NUMBER OF SEQUENCES: 169
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;; STREET: 500 West Madison Street, 34th floor
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: USA
;; ZIP: 60661
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/477,484B
;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION: 530
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/425,336
;; FILING DATE: 18-APR-1995
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/064,691
;; FILING DATE: 12-MAY-1993
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/988,430
;; FILING DATE: 09-DEC-1992
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/901,707
;; FILING DATE: 19-JUN-1992
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/787,567
;; FILING DATE: 04-NOV-1991
;;
;; ATTORNEY/AGENT INFORMATION:
;; NAME: McNicholas, Janet M.
;; REGISTRATION NUMBER: 32,918
;; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312/707-8889
;; TELEFAX: 312/707-9155
;; TELEX: 650 388-1248
;;
;; INFORMATION FOR SEQ ID NO: 100:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 251 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-477-484B-100

Query Match 99.7%; Score 1273; DB 1; Length 251;
Best Local Similarity 99.6%; Pred. No. 2.5e-118;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLDTSVSTKATYITVYVNFNLRLVKLPKGNHSHGIPLLRKKADDPKAPVLVNSDN 60
Db 1 GLDTSVSTKATYITVYVNFNLRLVKLPKGNHSHGIPLLRKKADDPKAPVLVNSDN 60

Qy 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKADPAAYEGLFKNTIKTRLHFGSYPSSLEGEK 120
Db 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKADPAAYEGLFKNTIKTRLHFGSYPSSLEGEK 120

Qy 121 AYRETTDLGIEPLRIGIKKLDENADINYPKTEIASLLVVIQWSEAAARFTFIENQIRNN 180
Db 121 AYRETTDLGIEPLRIGIKKLDENADINYPKTEIASLLVVIQWSEAAARFTFIENQIRNN 180

Qy 181 FQQRIRPANNITISLENKWKLSFOIRTSYGANGMFSSEAVELERANGKYYVTVAVDQVKPKI 240
Db 181 FQQRIRPANNITISLENKWKLSFOIRTSYGANGMFSSEAVELERANGKYYVTVAVDQVKPKI 240

Qy 241 ALLKFEVDKPK 251
Db 241 ALLKFEVDKPK 251

RESULT 15
US-08-646-360-99
;; Sequence 99, Application US/08646360
;; Patent No. 5837491
;; GENERAL INFORMATION:
;; APPLICANT: Better, Marc D.
;; APPLICANT: Carroll, Stephen F.
;; APPLICANT: Studnika, Gary M.
;; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;; TITLE OF INVENTION: Proteins
;; NUMBER OF SEQUENCES: 173
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;; STREET: 500 West Madison Street, 34th floor
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: USA
;; ZIP: 60661
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/646,360
;; FILING DATE: 13-MAY-1996
;; CLASSIFICATION: 530
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US94/05348
;; FILING DATE: 12-MAY-1994
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/064,691
;; FILING DATE: 12-MAY-1993
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/988,430
;; FILING DATE: 09-DEC-1992
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/901,707
;; FILING DATE: 19-JUN-1992
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/787,567
;; FILING DATE: 04-NOV-1991
;;
;; ATTORNEY/AGENT INFORMATION:
;; NAME: McNicholas, Janet M.
;; REGISTRATION NUMBER: 32,918
;; REFERENCE/DOCKET NUMBER: 200-70.P4
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312/707-8889
;; TELEFAX: 312/707-9155
;; TELEX: 650 388-1248
;;
;; INFORMATION FOR SEQ ID NO: 99:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 251 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-646-360-99

Query Match 99.7%; Score 1273; DB 1; Length 251;
Best Local Similarity 99.6%; Pred. No. 2.5e-118;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLDTSVSTKATYITVYVNFNLRLVKLPKGNHSHGIPLLRKKADDPKAPVLVNSDN 60
Db 1 GLDTSVSTKATYITVYVNFNLRLVKLPKGNHSHGIPLLRKKADDPKAPVLVNSDN 60

Qy 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKADPAAYEGLFKNTIKTRLHFGSYPSSLEGEK 120
Db 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKADPAAYEGLFKNTIKTRLHFGSYPSSLEGEK 120

Qy 121 AYRETTDLGIEPLRIGIKKLDENADINYPKTEIASLLVVIQWSEAAARFTFIENQIRNN 180

Db	121	AYRETTDLGIEPLRIGIKKLDENAI	DNYKPT	EIASLLVVIQWSEARFTFIENQIRNN	180
Qy	181	FQORIRPANNTISLENKWKLSFQIRTS	GANGMFSEAV	ELERANGKYYVTAVDQVKPKI	240
Db	181	FQORIRPANNTISLENKWKLSFQIRTS	GANGMFSEAV	ELERANGKYYVTAVDQVKPKI	240
Qy	241	ALLKFVDKDPK	251		
Db	241	ALLKFVDKDPK	251		

Search completed: February 10, 2006, 10:15:59
Job time : 51.0148 secs

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OM protein - protein search, using sw model

Run on: February 10, 2006, 10:00:34 ; Search time 212.1 Seconds
(without alignments)
834.927 Million cell updates/sec

Title: US-10-717-243-2

Perfect score: 1287

Sequence: 1 GLDTVSFTKATYTYNFF.....AVDQVKPKALLKFVDKDPK 251

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trenbl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1287	100.0	316	1	RIPG_GELMU
2	1242.5	96.5	258	2	Q9S9E4_GELMU
3	394.5	30.7	581	2	Q94BW5_CINCA
4	393.5	30.6	580	2	Q94BW3_CINCA
5	392.5	30.5	549	2	Q9FV22_CINCA
6	388	30.1	299	2	Q8GZN9_9ROSI
7	386.5	30.0	580	2	Q94BW4_CINCA
8	361.5	28.1	563	2	Q8GT32_SAMNI
9	357.5	27.8	297	2	Q8GZP0_9ROSI
10	352	27.4	563	1	NTGB_SAMNI
11	352	27.4	563	2	Q945S2_SAMNI
12	348.5	27.1	563	2	Q04367_SAMNI
13	346	26.9	264	2	Q884J5_MOMCH
14	346	26.9	286	1	RIP2_MOMBA
15	346	26.9	286	1	RIP3_MOMCH
16	346	26.9	286	1	QSPZ05_MOMCH
17	344	26.7	541	2	Q41174_RICCO
18	343	26.7	576	1	RICI_RICCO
19	341.5	26.5	265	1	RIP2_PHYDI
20	338.5	26.3	294	1	RIP1_TRIAN
21	337.5	26.2	564	2	Q9AVR2_9DIPS
22	334.5	26.0	564	1	AGGL_RICCO
23	333.5	25.9	527	1	ABRB_ABRPR
24	333	25.9	282	1	RIP2_BRYDI
25	330.5	25.7	294	1	RIPA_PHYAM
26	329	25.6	252	2	Q38760_ABRPR
27	327.5	25.4	294	2	Q8YU01_9ROSI
28	327.5	25.4	294	2	Q8YU01_9ROSI
29	325.5	25.3	275	2	Q84LJ1_GYNPE
30	325	25.3	313	1	RIP1_PHYAM
31	325	25.3	313	2	Q6PWU4_PHYAM

32	325	25.3	313	2	Q53YN2_PHYAM	Q53yn2 phytolacca
33	324.5	25.2	277	2	Q84JRI_GYNPE	Q84jri gynostemma
34	324.5	25.2	293	2	Q8S452_9ROSI	Q8s452 jatropa cu
35	324	25.2	289	2	Q41216_TRIKI	Q41216 trichosan
36	323.5	25.1	277	2	Q8GV09_GYNPE	Q8gv09 gynostemma
37	322.5	25.1	275	2	Q8H1Y4_GYNPE	Q8h1y4 gynostemma
38	322.5	25.1	298	2	Q5F0I3_GYNPE	Q5f0i3 gynostemma
39	321	24.9	289	1	RIP1_TRIKI	P09989 trichosan
40	321	24.9	289	2	Q94KE4_TRIKI	Q94ke4 trichosan
41	321	24.9	567	2	Q6H267_VISAL	Q6h267 viscum albu
42	320.5	24.9	277	2	Q8GV11_GYNPE	Q8gv11 gynostemma
43	320.5	24.9	565	2	Q04071_SAMNI	Q04071 sambucus ni
44	320	24.9	251	2	Q7DM12_ABRPR	Q7dm12 abrus preca
45	320	24.9	252	2	Q38761_ABRPR	Q38761 abrus preca

ALIGNMENTS

RESULT 1

ID	RIPG_GELMU	STANDARD;	PRT;	316 AA.
AC	P33186;			
DT	01-OCT-1993	(Rel. 27, Created)		
DT	01-NOV-1995	(Rel. 32, Last sequence update)		
DT	10-MAY-2005	(Rel. 47, Last annotation update)		
DE	Ribosome-inactivating protein gelonin precursor (EC 3.2.2.22) (rRNA N-glycosidase).			
CN	Name=GELN;			
OS	Gelonium multiflorum (Euphorbiaceae himalaya).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;			
OC	rosids; eurosids I; Malpighiales; Euphorbiaceae; Crotonoideae;			
OC	Geloneae; Gelonium.			
OX	NCBI_TaxID=3979;			
RP	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=94085781; PubMed=7916721; DOI=10.1016/0378-1119(93)90097-M;			
RA	Nolan P.A., Garrison D.A., Better M.;			
RT	"Cloning and expression of a gene encoding gelonin, a ribosome-inactivating protein from Gelonium multiflorum.";			
RL	Gene 134:223-227(1993).			
RL	[2]			
RP	PROTEIN SEQUENCE OF 47-93.			
RP	TISSUE=Seed;			
RX	MEDLINE=89326691; PubMed=2753596;			
RA	Montecucchi P.-C., Lazzarini A.M., Barbieri L., Stirpe F., Soria M.,			
RA	Lappi D.;			
RT	"N-terminal sequence of some ribosome-inactivating proteins.";			
RL	Int. J. Pept. Protein Res. 33:263-267(1989).			
RL	[3]			
RP	X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).			
RX	MEDLINE=95333189; PubMed=7608981;			
RA	Hosur M.V., Nair B., Satyamurthy P., Misquith S., Surolia A.,			
RA	Kannan K.K.;			
RT	"X-ray structure of gelonin at 1.8-A resolution.";			
RL	J. Mol. Biol. 250:368-380(1995).			
CC	- - CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.			
CC	- - SUBUNIT: Homodimer.			
CC	- - SIMILARITY: Belongs to the ribosome-inactivating protein family.			
CC	Type 1 RIP subfamily.			
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.			
CC	EMBL; L12243; AAA16312.1; -; mRNA.			
DR	PIR; JT0753; JT0753.			
DR	HSSP; P09989; IMRJ.			
DR	InterPro; IPR001574; RIP.			

DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN
DR PROSITE; PS00275; SHIGA_RICIN; 1.
KW Direct protein sequencing; Glycoprotein; Hydrolase; Plant defense;
KW Protein synthesis inhibitor; Signal; Toxin.
FT SIGNAL 1 26 Potential.
FT PROPEP 27 46
FT CHAIN 47 297 Ribosome-inactivating protein gelonin.
FT PROPEP 298 316 Removed in mature form.
FT ACT SITE 212 212
FT CARBOHYD 235 235 N-linked (GlcNAc. . .).
FT DISULFID 90 96 C -> K (in Ref. 2).
FT CONFLICT 90 90 P -> D (in Ref. 2).
FT CONFLICT 93 93
SQ SEQUENCE 316 AA; 35419 MW; 1252F3E710901B85 CRC64;
Query Match 100.0%; Score 1287; DB 1; Length 316;
Best Local Similarity 100.0%; Pred. No. 5.3e-100;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLDTSVSTKGTATITTYVNFNLNLRVVKLPKPGNSHGIPLLRKKDDPGKCFVLVALSNDN 60
47 GLDTSVSTKGTATITTYVNFNLNLRVVKLPKPGNSHGIPLLRKKDDPGKCFVLVALSNDN 106
QY 61 GOLAEIAIDVTSVYVVGQVNRNSYFFKDAADAAVEGLFKNTIKTRLHFGSGPSLEGEK 120
107 GOLAEIAIDVTSVYVVGQVNRNSYFFKDAADAAVEGLFKNTIKTRLHFGSGPSLEGEK 166
QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQWSEAAARFTFENQIRNN 180
167 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQWSEAAARFTFENQIRNN 226
QY 181 FQOIRPNNTISLENKKGKLSFQIRTSANGMFSEAVELERANGKYYTAVDQVKPKI 240
227 FQOIRPNNTISLENKKGKLSFQIRTSANGMFSEAVELERANGKYYTAVDQVKPKI 286
QY 241 ALLKFVDKDPK 251
DB 287 ALLKFVDKDPK 297
RESULT 2
ID Q9S9B4_GELMU PRELIMINARY; PRT; 258 AA.
AC Q9S9E4;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE rRNA -glycosidase (EC 3.2.2.22) (rRNA N-glycosidase).
OS Gelonium multiflorum (Euphorbiaceae himalayana).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids I; Malpighiales; Euphorbiaceae; Crotonoideae;
OC Geloniaeae; Gelonium.
OX NCBI_TaxID=3979;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=96006751; PubMed=7553224;
RA Rosenblum M.G., Kohr W.A., Beattie K.L., Beattie W.G., Marks W.,
RA Toman P.D., Cheung L.;
RT "Amino acid sequence analysis, gene construction, cloning, and
RT expression of Gelonin, a toxin derived from Gelonium multiflorum.";
RL J. Interferon Cytokine Res. 15:547-555 (1995).
DR HSP; P09989; 1MRJ.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0037148; P:negative regulation of protein biosynthesis; IEA.
DR GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR PROSITE; PS00275; SHIGA_RICIN; 1.

KW Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.
SQ SEQUENCE 258 AA; 28826 MW; 13D68B673F4D6B06 CRC64;
Query Match 96.5%; Score 1242.5; DB 2; Length 258;
Best Local Similarity 95.8%; Pred. No. 2.3e-96;
Matches 248; Conservative 1; Mismatches 1; Indels 9; Gaps 2;
QY 1 GLDTSVSTKGTATITTYVNFNLNLRVVKLPKPGNSHGIPLLRKKDDPGKCFVLVALSNDN 60
DB 1 GLDTSVSTKGTATITTYVNFNLNLRVVKLPKPGNSHGIPLLRKKDDPGKCFVLVALSNDN 59
QY 61 GOLAEIAIDVTSVYVVGQVNRNSYFFKDAADAAVEGLFKNTIKTRLHFGSGPS 112
60 GOLAEIAIDVTSVYVVGQVNRNSYFFKDAADAAVEGLFKNTIKTNKPLFGKTRLHFGSG 119
QY 113 YPSLEGEKAYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQWSEAAARFTF 172
120 YPSLEGEKAYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQWSEAAARFTF 179
QY 173 IENQIRNPFQOIRPNNTISLENKKGKLSFQIRTSANGMFSEAVELERANGKYYTAV 232
180 IENQIRNPFQOIRPNNTISLENKKGKLSFQIRTSANGMFSEAVELERANGKYYTAV 239
QY 233 VDQVKPKIALLKFDKDPK 251
DB 240 VDQVKPKIALLKFDKDPK 258
RESULT 3
ID Q94BW5_CINCA PRELIMINARY; PRT; 581 AA.
AC Q94BW5;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Type 2 ribosome-inactivating protein cinnamomin I precursor.
OS Cinnamomum camphora (Camphor tree).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; magnoliids; Laurales; Lauraceae;
OC Cinnamomum.
OX NCBI_TaxID=13429;
RN [1]
RP NUCLEOTIDE SEQUENCE.
EX MEDLINE=21888636; PubMed=11891062; DOI=10.1016/S0378-1119(01)00890-3;
RA Yang Q., Liu R.S., Cong Z.Z., Liu W.Y.;
RT "Studies of three genes encoding Cinnamomin (a type II RIP) isolated
RT from the seeds of camphor tree and their expression patterns.";
RL Gene 284:215-223 (2002).
DR EMBL; AY039801; AAK82458.1; -; Genomic_DNA.
DR HSP; P02879; 2AAI.
DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR InterPro; IPR000772; Ricin_B_lectin.
DR InterPro; IPR001574; Ricin.
DR Pfam; PF00652; Ricin_B_lectin; 2.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR SMART; SM00458; RICIN; 2.
DR PROSITE; PS50231; RICIN_B_LECTIN; 2.
KW SIGNAL.
FT SIGNAL 1 32 Potential.
FT CHAIN 33 581 type 2 ribosome-inactivating protein
FT cinnamomin I.
SQ SEQUENCE 581 AA; 64215 MW; 6E8F5F8FEA3D196 CRC64;
Query Match 30.7%; Score 394.5; DB 2; Length 581;
Best Local Similarity 39.7%; Pred. No. 1.8e-24;
Matches 100; Conservative 45; Mismatches 94; Indels 13; Gaps 8;
QY 4 TVSFSTKGTATITTYVNFNLNLRVVKLPKPGNSHGIPLLRKKDDPGKCFVLVALSNDN 59
35 TVTFSTKGTATITTYVNFNLNLRVVKLPKPGNSHGIPVNRERSTVPDSKRFILVELSNWAAD 94

from the seeds of camphor tree and their expression patterns.";

RT Gene 284:215-223(2002).
DR EMBL; AY039802; AAK82459.1; -; Genomic_DNA.
DR HSSP; P02879; 2AAI.
DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR InterPro; IPR000772; Ricin_B_lectin.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00652; Ricin_B_lectin; 2.
DR Pfam; PF00161; RIP_1.
DR PRINTS; PR00396; SHIGARICIN.
DR SMART; SM00458; RICIN; 2.
DR PROSITE; PS0231; RICIN_B_LECTIN; 2.
KW SIGNAL.
FT FT
FT CHAIN 1 32 Potential.
FT 33 580 type 2 ribosome-inactivating protein
FT cinnamomin II.
SQ SEQUENCE 580 AA; 64265 MW; 37E4289ECCE0CBFF CRC64;

Query Match 30.0%; Score 386.5; DB 2; Length 580;
Best Local Similarity 39.8%; Pred.No.8.5e-24;
Matches 101; Conservative 43; Mismatches 93; Indels 17; Gaps 9;

QY 4 TVSFSTKGTATTYTNFLNELRVKLPGNSHGIPLLRKCDPP-GKCFVLVALSN---D 59
Db ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:|||||
35 TVTFTTKNATKTSYTOFIEALRAQLASGBEPHGPVMDRGSTVPDSKRFLIVLSNWAAD 94
QY 60 NQLGLABIAIDTVSVVVGVQVRNSRVSFPFK-DAPDAAYEGLFKNKTIKTRLHFSGSYPSLE- 117
Db ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:|||||
95 SP--VALAVDVVNAYVAVRTGQSFPFLREDNPDPAIENLLPTKKYTPFPFGSYTDLER 152
QY 118 --GEKAYRETDLGIPLRIGIKLDENAIIDNYKPTEIASLIIVIQMVSEAAARFTPIEN 175
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
153 VAGE--LRREILLEGMPLENALSALTWSNLNQQR--ALARSLLIVLQWAEAVRFRIEY 208
QY 176 QIRNNF--QOIRPANNTISLENKGKLSFQIRTSGANGWFSSAEVLERANGKKYYVTAV 233
Db ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:|||||
209 RVRESITRAEMRPDPAMLSLENKWSALSNAVQQSGGVFSFSPVELRSINKPVVVGVS 268
QY 234 -DOVKPKIALLKPFV 246
Db ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:|||||
269 SDRVISGLAIMLFI 282

RESULT 8
QG8T32_SAMNI PRELIMINARY; PRT; 563 AA.
AC AC
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Type 2 ribosome-inactivating protein Nigirin 1 (EC 3.2.2.22).
OS Sambucus nigra (European elder).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asteride;
OC Campanulids; Dipsacales; Adoxaceae; Sambucaceae; Sambucus.
OX NCBI_TaxID=4202;
RN RN
NP NUCLEOTIDE SEQUENCE.
RC TISSUE=Leaf;
RC Gibbs T., Arias F.J., Antolin P.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AP249280; AAN86130.1; -; mRNA.
DR HSSP; Q9AVR2; 1HW.
DR SNR; Q8GT32; 26-274, 299-560.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR InterPro; IPR000772; Ricin_B_lectin.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00652; Ricin_B_lectin; 2.
DR Pfam; PF00161; RIP; 1.

DR	Pfam; PF00652; Ricin_B_lectin; 2.	FT	CHAIN	2	264	type I ribosome inactivating protein.
DR	Pfam; PF00161; RIP; 1.	FT	NON_TER	1	1	
DR	PRINTS; PR00396; SHIGARICIN.	SQ	SEQUENCE	264 AA; 29775 MW; AD9B1175B70521AD	CRC64;	
DR	SMART; SM00458; RICIN; 2.					
DR	PROSITE; PS0231; RICIN_B_LECTIN; 2.					
DR	PROSITE; PS00275; SHIGA_RICIN; 1.					
KW	SIGNAL.					
FT	SIGNAL	1	25	Potential.		
FT	CHAIN	26	297	ribosome inactivating protein, A chain.		
FT	CHAIN	298	563	ribosome inactivating protein, B chain.		
SQ	SEQUENCE	563 AA; 62336 MW; 3ED2B6C08E76205	CRC64;			
	Query Match	27.1%;	Score 348.5;	DB 2;	Length 563;	
	Best Local Similarity	39.7%;	Pred. No. 1.3e-20;			
	Matches	91;	Conservative	36;	Mismatches	87;
					Indels	15;
					Gaps	7;
QY	1	GLD--TVSPSTKATVITYVNFNLRL-VKLKPEGNSHGIPLLRKKDDPGK-CFVLVAL	56			
DB	25	GIDYPSVSNLAGAKSATYRDFLKNLRTIVATGTYVNGLPVIRKSEVQVKNRFLVLL	84			
QY	57	SNNDGQLABIAIDVTSVYVGVQVNRNSYFFKDAADAAVEGLFKNTIKTRLHFGSGYPSL	116			
DB	85	TNYNGNTVTLAVDVTNLYVVAESANANSYFFKDAATQLOKSNLFVGTQHTLPFTGNYDL	144			
QY	117	E-GEKAYRETTDLCIGLEPLRIGIKLDENAIIDNYKTEIASSLLVVIQVMSAARFTFEN	175			
DB	145	ETAAGTRRESIELGPSPLDGAITSL-----YDESVAESLLVVIQVMSAARFRYIEQ	197			
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DB	198	EVRRSLQQTAGTFPNALMUSMENNSSMSLEVRQSGDNVSPFTGTVLQ	246			
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ID	Q684J5_MONCH PRELIMINARY;	PRT;	264 AA.			
AC	Q684J5;					
DT	25-OCT-2004 (T-EMBLrel. 28, Created)					
DT	25-OCT-2004 (T-EMBLrel. 28, Last sequence update)					
DT	25-OCT-2004 (T-EMBLrel. 28, Last annotation update)					
DE	Type I ribosome inactivating protein precursor (Fragment).					
GN	Name-rp;					
OS	Momordica charantia (Bitter gourd) (Balsam pear).					
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;					
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;					
OC	rosids; eurosids I; Cucurbitales; Cucurbitaceae; Momordica.					
OX	NCBI_TaxID=3673;					
RN	[1]					
RP	NUCLEOTIDE SEQUENCE.					
RC	STRAIN=HN1;					
RA	Nguyen Dinh C., Nguyen Thuy D., Le Thi Thu H., Nguyen Huy H.,					
RA	Tran Thi Phuong L., Nong Van H.;					
RT	"Expression of a gene encoding ribosome inactivating protein from					
RT	bitter melon (Momordica charantia).";					
RL	Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.					
CC	[2]					
RN	NUCLEOTIDE SEQUENCE.					
RC	STRAIN=HN1;					
RA	Nong V.;					
RL	Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.					
RL	EMBL; AJ748278; CAH19208.1; -; Genomic_DNA.					
DR	SMR; Q684J5; 2-264.					
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DR	GO; GO:0030598; P:RNA N-glycosylase activity; IEA.					
DR	GO; GO:0006952; P:defense response; IEA.					
DR	GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.					
DR	GO; GO:0009405; P:pathogenesis; IEA.					
DR	InterPro; IPR001574; RIP.					
DR	Pfam; PF00161; RIP; 1.					
DR	PRINTS; PR00396; SHIGARICIN.					
DR	PROSITE; PS00275; SHIGA_RICIN; 1.					
DR	Hydrolase; Plant defense; Protein synthesis inhibitor; Signal; Toxin.					
KW	SIGNAL	<1	1	Potential.		
FT	CHAIN	264	286	Ribosome-inactivating protein momordin		
FT	SIGNAL	1	1	II.		

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 10, 2006, 10:13:09 ; Search time 50.0148 Seconds
(without alignments)
414.909 Million cell updates/sec

Title: US-10-717-243-2

Perfect score: 1287

Sequence: 1 GLDTSFSTKGATYYTNNF.....AVDQVKPKIALKFFVDKPK 251

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA:*

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2: /cgn2_6/ptodata/1/1aa/6 COMB.pep.*
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6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1287	100.0	251	1 US-08-488-113B-2	Sequence 2, Appli
3	1287	100.0	251	1 US-08-477-484B-2	Sequence 2, Appli
4	1287	100.0	251	1 US-08-646-360-2	Sequence 2, Appli
5	1287	100.0	251	1 US-08-621-803-247	Sequence 247, App
6	1287	100.0	251	2 US-08-839-765-2	Sequence 2, Appli
7	1287	100.0	251	2 US-09-136-389-2	Sequence 2, Appli
8	1287	100.0	251	2 US-09-217-352-247	Sequence 247, App
9	1287	100.0	251	2 US-09-610-838-2	Sequence 2, Appli
10	1287	100.0	251	2 US-09-711-485-2	Sequence 2, Appli
11	1287	100.0	251	2 US-09-645-603B-2	Sequence 2, Appli
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13	1284	99.8	251	1 US-07-988-430-2	Sequence 2, Appli
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31	1279	99.4	251	1 US-08-425-336-105	Sequence 105, App
32	1279	99.4	251	1 US-08-425-336-106	Sequence 106, App
33	1279	99.4	251	1 US-08-425-336-109	Sequence 109, App
34	1279	99.4	251	1 US-08-488-113B-103	Sequence 103, App
35	1279	99.4	251	1 US-08-488-113B-104	Sequence 104, App
36	1279	99.4	251	1 US-08-488-113B-105	Sequence 105, App
37	1279	99.4	251	1 US-08-488-113B-106	Sequence 106, App
38	1279	99.4	251	1 US-08-488-113B-109	Sequence 109, App
39	1279	99.4	251	1 US-08-477-484B-103	Sequence 103, App
40	1279	99.4	251	1 US-08-477-484B-104	Sequence 104, App
41	1279	99.4	251	1 US-08-477-484B-105	Sequence 105, App
42	1279	99.4	251	1 US-08-477-484B-106	Sequence 106, App
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ALIGNMENTS

RESULT 1

US-08-425-336-2
; Sequence 2, Application US/08425336
; Patent No. 5621083
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroli, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/425,336
; APPLICATION NUMBER: US/08/425,336
; FILING DATE: 18-APR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Thomas C.
; REGISTRATION NUMBER: P-36,989
; REFERENCE/DOCKET NUMBER: 31394
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-425-336-2

Query Match 100.0%; Score 1287; DB 1; Length 251;
Best Local Similarity 100.0%; Pred. No. 1.2e-124; Mismatches 0; Gaps 0;
Matches 251; Conservative 0; Indels 0; Gaps 0;

QY 1 GLDVSFSTKGATITTYVNFNLRLVKLPKPGNSHGIPLLRKKDDPGKCFVLVALSNDN 60
DB 1 GLDVSFSTKGATITTYVNFNLRLVKLPKPGNSHGIPLLRKKDDPGKCFVLVALSNDN 60

QY 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGGSSPSLEGEK 120
DB 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGGSSPSLEGEK 120

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DB 121 AYRETTDLGIEPLRIGIKLDENADNYKPTIEASLLVVIQWSEAAARFTFIENQIRNN 180

QY 181 FQORIRPANNTISLENKWGKLSFOIRTSGANGMFSEAVELERANGKYYVTAVDQVKPKI 240
DB 181 FQORIRPANNTISLENKWGKLSFOIRTSGANGMFSEAVELERANGKYYVTAVDQVKPKI 240

QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 2

US-08-488-113B-2
; Sequence 2, Application US/08488113B
; Patent No. 5744580
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,113B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-488-113B-2

Query Match 100.0%; Score 1287; DB 1; Length 251;
Best Local Similarity 100.0%; Pred. No. 1.2e-124; Mismatches 0; Gaps 0;
Matches 251; Conservative 0; Indels 0; Gaps 0;

QY 1 GLDVSFSTKGATITTYVNFNLRLVKLPKPGNSHGIPLLRKKDDPGKCFVLVALSNDN 60
DB 1 GLDVSFSTKGATITTYVNFNLRLVKLPKPGNSHGIPLLRKKDDPGKCFVLVALSNDN 60

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DB 181 FQORIRPANNTISLENKWGKLSFOIRTSGANGMFSEAVELERANGKYYVTAVDQVKPKI 240

QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 3

US-08-477-484B-2
; Sequence 2, Application US/08477484B
; Patent No. 5756699
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,484B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-477-484B-2

Query Match 100.0%; Score 1287; DB 1; Length 251;
Best Local Similarity 100.0%; Pred. No. 1.2e-124;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKADPAAYEGLFKNTIKTRLHFGSGSYPSLEGK 120
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DB 241 ALLKFVDKDPK 251

RESULT 4

US-08-646-360-2
Sequence 2, Application US/08646360
Patent No. 5837491
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen P.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSER: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-646-360-2

Query Match 100.0%; Score 1287; DB 1; Length 251;
Best Local Similarity 100.0%; Pred. No. 1.2e-124;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 121 AYRETTDLGIEPLRIGIKLDENADNYKPTIASLLVVIQWVSEAAARFTFIENQIRNN 180
QY 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFMSEAVELERANGKYYVTAVDQVKPKI 240
DB 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFMSEAVELERANGKYYVTAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 5

US-08-621-803-247
Sequence 247, Application US/08621803
Patent No. 5851802
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
TITLE OF INVENTION: Methods for Recombinant Microbial Production of
TITLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:


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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/621,803
; FILING DATE: 22-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 247:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-621-803-247

Query Match 100.0%; Score 1287; DB 1; Length 251;
Best Local Similarity 100.0%; Pred. No. 1.2e-124; Mismatches 0; Indels 0; Gaps 0;
Matches 251; Conservative 0;

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Db 1 GLDVSFSTKGATITVYNFLNELRVKLKPGNSHGIPLLRKKDDPGKCFVLVALSNDN 60

QY 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKADPAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
Db 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKADPAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120

QY 121 AYRETTDLGIEPLRIGIKLDENADNYKPTIASSLLVVIQWSEAAARFTFIENQIRNN 180
Db 121 AYRETTDLGIEPLRIGIKLDENADNYKPTIASSLLVVIQWSEAAARFTFIENQIRNN 180

QY 181 FOQIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
Db 181 FOQIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240

QY 241 ALLKFVDKDPK 251
Db 241 ALLKFVDKDPK 251

RESULT 6
US-08-839-765-2
; Sequence 2, Application US/08839765
; Patent No. 6146631
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/839,765

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; FILING DATE: 15-APR-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-839-765-2

Query Match 100.0%; Score 1287; DB 2; Length 251;
Best Local Similarity 100.0%; Pred. No. 1.2e-124;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLDVSFSTKGATITVYNFLNELRVKLKPGNSHGIPLLRKKDDPGKCFVLVALSNDN 60
Db 1 GLDVSFSTKGATITVYNFLNELRVKLKPGNSHGIPLLRKKDDPGKCFVLVALSNDN 60

QY 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKADPAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
Db 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKADPAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120

QY 121 AYRETTDLGIEPLRIGIKLDENADNYKPTIASSLLVVIQWSEAAARFTFIENQIRNN 180
Db 121 AYRETTDLGIEPLRIGIKLDENADNYKPTIASSLLVVIQWSEAAARFTFIENQIRNN 180

QY 181 FOQIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
Db 181 FOQIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240

QY 241 ALLKFVDKDPK 251
Db 241 ALLKFVDKDPK 251

RESULT 7
US-09-136-389-2
; Sequence 2, Application US/09136389
; Patent No. 6146850
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago

```


STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/136,389
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-136-389-2

Query Match 100.0%; Score 1287; DB 2; Length 251;
Best Local Similarity 100.0%; Pred. No. 1.2e-124; Indels 0; Gaps 0;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLDVSFSTKGATYTYVNFNLRLVKLPKGNHGIPLLRKCKDDPGKCFVLVSLNDN 60
DB 1 GLDVSFSTKGATYTYVNFNLRLVKLPKGNHGIPLLRKCKDDPGKCFVLVSLNDN 60
QY 61 GOLAEIAIDVTSVYVGVQVNRYSFFKADPDAAYEGLFKNTIKTRLHFGSGYPSLEGEK 120
DB 61 GOLAEIAIDVTSVYVGVQVNRYSFFKADPDAAYEGLFKNTIKTRLHFGSGYPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKLDENADNYKPTIEASLLVVIOMVSEAAARFTFIENQIRN 180
DB 121 AYRETTDLGIEPLRIGIKLDENADNYKPTIEASLLVVIOMVSEAAARFTFIENQIRN 180
QY 181 FQQRIRPANNTISLENKWKLSFQIRTSANGMFMSEAVELERANGKYYVTAVDQVKPKI 240
DB 181 FQQRIRPANNTISLENKWKLSFQIRTSANGMFMSEAVELERANGKYYVTAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 8
US-09-217-352-247
; Sequence 247, Application US/09217352

Patent No. 6274344
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
TITLE OF INVENTION: Methods for Recombinant Microbial Production of Fusion Proteins and BPI-Derived Peptides
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/217,352
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/621,803
FILING DATE: 22-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 27129/33199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 247:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-217-352-247

Query Match 100.0%; Score 1287; DB 2; Length 251;
Best Local Similarity 100.0%; Pred. No. 1.2e-124; Indels 0; Gaps 0;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLDVSFSTKGATYTYVNFNLRLVKLPKGNHGIPLLRKCKDDPGKCFVLVSLNDN 60
DB 1 GLDVSFSTKGATYTYVNFNLRLVKLPKGNHGIPLLRKCKDDPGKCFVLVSLNDN 60
QY 61 GOLAEIAIDVTSVYVGVQVNRYSFFKADPDAAYEGLFKNTIKTRLHFGSGYPSLEGEK 120
DB 61 GOLAEIAIDVTSVYVGVQVNRYSFFKADPDAAYEGLFKNTIKTRLHFGSGYPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKLDENADNYKPTIEASLLVVIOMVSEAAARFTFIENQIRN 180
DB 121 AYRETTDLGIEPLRIGIKLDENADNYKPTIEASLLVVIOMVSEAAARFTFIENQIRN 180
QY 181 FQQRIRPANNTISLENKWKLSFQIRTSANGMFMSEAVELERANGKYYVTAVDQVKPKI 240
DB 181 FQQRIRPANNTISLENKWKLSFQIRTSANGMFMSEAVELERANGKYYVTAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 9
US-09-610-838-2
; Sequence 2, Application US/09610838
; Patent No. 6376217
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.


```

; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/610,838
; FILING DATE: 06-JUL-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/136,389
; FILING DATE: 18-AUG-1998
; APPLICATION NUMBER: 08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-610-838-2

Query Match 100.0%; Score 1287; DB 2; Length 251;
Best Local Similarity 100.0%; Pred. No. 1.2e-124;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLDTSFSTKGATITTYVNFNLRLVKLPKPNHSHGIPLLRKKDDPGKCFVLVALSNDN 60
Db 1 GLDTSFSTKGATITTYVNFNLRLVKLPKPNHSHGIPLLRKKDDPGKCFVLVALSNDN 60

QY 61 GQLAEIAIDVTSVVGVQVRNRSYFFKADPAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
Db 61 GQLAEIAIDVTSVVGVQVRNRSYFFKADPAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120

QY 121 AYRETTDLGIEPLRIGIKKLDENADNYPKPTIASLLVVIQWSEARFTFIENQIRNN 180
Db 121 AYRETTDLGIEPLRIGIKKLDENADNYPKPTIASLLVVIQWSEARFTFIENQIRNN 180

QY 181 FOQRTRPANNTISLENKWKGLSFQIRTSANGWFSSEAVELEKNGKYYVTVADQVKPKI 240
Db 181 FOQRTRPANNTISLENKWKGLSFQIRTSANGWFSSEAVELEKNGKYYVTVADQVKPKI 240
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QY 241 ALLKFVDKDPK 251
Db 241 ALLKFVDKDPK 251

RESULT 10
US-09-711-485-2
; Sequence 2, Application US/09711485
; Patent No. 6649742
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/09/711,485
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/839,765
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-711-485-2

Query Match 100.0%; Score 1287; DB 2; Length 251;
Best Local Similarity 100.0%; Pred. No. 1.2e-124;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLDTSFSTKGATITTYVNFNLRLVKLPKPNHSHGIPLLRKKDDPGKCFVLVALSNDN 60
Db 1 GLDTSFSTKGATITTYVNFNLRLVKLPKPNHSHGIPLLRKKDDPGKCFVLVALSNDN 60

QY 61 GQLAEIAIDVTSVVGVQVRNRSYFFKADPAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
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Db 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKADPAAYEGLFKNTIKTRLHFGGSPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTIEASLLVVIQWSEAAARFTFIENQIRNN 180
Db 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTIEASLLVVIQWSEAAARFTFIENQIRNN 180
QY 181 FQOIRPANNTISLENKWGKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240
Db 181 FQOIRPANNTISLENKWGKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240
QY 241 ALLKPFVDKPK 251
Db 241 ALLKPFVDKPK 251

RESULT 11
US-09-645-603B-2
; Sequence 2, Application US/09645603B
; Patent No. 6652861
; GENERAL INFORMATION:
; APPLICANT: LEE-HUANG, Sylvia
; TITLE OF INVENTION: Anti-HIV and Anti-tumor Peptides and Truncated Polypeptides of
; FILE REFERENCE: map30 and gap31
; CURRENT APPLICATION NUMBER: US/09/645,603B
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/150,885
; PRIOR FILING DATE: 1999-08-26
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 2
; TYPE: PRT
; ORGANISM: Gelonium multiflorum
US-09-645-603B-2

Query Match 100.0%; Score 1287; DB 2; Length 251;
Best Local Similarity 100.0%; Pred. No. 1.2e-124;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLDTSVSTKGATYTYVNFNLRLVKLPKGNHSHGIFLLRKKDDPGKCFVLVALSNDN 60
Db 1 GLDTSVSTKGATYTYVNFNLRLVKLPKGNHSHGIFLLRKKDDPGKCFVLVALSNDN 60
QY 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKADPAAYEGLFKNTIKTRLHFGGSPSLEGEK 120
Db 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKADPAAYEGLFKNTIKTRLHFGGSPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTIEASLLVVIQWSEAAARFTFIENQIRNN 180
Db 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTIEASLLVVIQWSEAAARFTFIENQIRNN 180
QY 181 FQOIRPANNTISLENKWGKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240
Db 181 FQOIRPANNTISLENKWGKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240
QY 241 ALLKPFVDKPK 251
Db 241 ALLKPFVDKPK 251

RESULT 12
US-07-901-707-2
; Sequence 2, Application US/07901707
; Patent No. 5376546
; GENERAL INFORMATION:
; APPLICANT: Bernhard, Susan L.
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Steve P.
; APPLICANT: Lane, Julie A.
; TITLE OF INVENTION: Materials Comprising and Methods of
; TITLE OF INVENTION: Composition and Use for Ribosome-Inactivating Proteins

NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/901,707
; FILING DATE: 19920619
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5376546and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27129/30910
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-5750
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-901-707-2
Query Match 99.8%; Score 1284; DB 1; Length 251;
Best Local Similarity 99.6%; Pred. No. 2.5e-124;
Matches 250; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLDTSVSTKGATYTYVNFNLRLVKLPKGNHSHGIFLLRKKDDPGKCFVLVALSNDN 60
Db 1 GLDTSVSTKGATYTYVNFNLRLVKLPKGNHSHGIFLLRKKDDPGKCFVLVALSNDN 60
QY 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKADPAAYEGLFKNTIKTRLHFGGSPSLEGEK 120
Db 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKADPAAYEGLFKNTIKTRLHFGGSPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTIEASLLVVIQWSEAAARFTFIENQIRNN 180
Db 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTIEASLLVVIQWSEAAARFTFIENQIRNN 180
QY 181 FQOIRPANNTISLENKWGKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240
Db 181 FQOIRPANNTISLENKWGKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240
QY 241 ALLKPFVDKPK 251
Db 241 ALLKPFVDKPK 251

RESULT 13
US-07-988-430-2
; Sequence 2, Application US/07988430
; Patent No. 5416202
; GENERAL INFORMATION:
; APPLICANT: Bernhard, Susan L.
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Lane, Julie A.
; APPLICANT: Lei, Shau-Ping

;; TITLE OF INVENTION: Materials Comprising and Methods of
;; TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins
;; NUMBER OF SEQUENCES: 101
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Marshhall, O'Toole, Gerstein, Murray &
;; ADDRESSEE: Bicknell,
;; STREET: Two First National Plaza, 20 South Clark
;; STREET: Street
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: USA
;; ZIP: 60603
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/988,430
;; FILING DATE: 19921209
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/901,707
;; FILING DATE: 19-JUN-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/787,567
;; FILING DATE: 04-NOV-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: No. 5416202and, Greta E.
;; REGISTRATION NUMBER: 35302
;; REFERENCE/DOCKET NUMBER: 31133
;; TELEPHONE: (312) 346-5750
;; TELEFAX: (312) 984-9740
;; TELEX: 25-3856
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 251 amino acids
;; TYPE: AMINO ACID
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-07-988-430-2

Query Match 99.8%; Score 1284; DB 1; Length 251;
Best Local Similarity 99.6%; Pred. No. 2.5e-124;
Matches 250; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLDTSFSTKGATYTYVNFNLRLVKLPKGNHGIPLLRKKDDPGKCFVLVALSNDN 60
DB 1 GLDTSFSTKGATYTYVNFNLRLVKLPKGNHGIPLLRKKDDPGKCFVLVALSNDN 60
QY 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
DB 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKL DENAIDNYKPTIEASLLVVIQWSEAAARFTFIEQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKL DENAIDNYKPTIEASLLVVIQWSEAAARFTFIEQIRNN 180
QY 181 FOQIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEERANGKYYVTAVDQVKPKI 240
DB 181 FOQIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEERANGKYYVTAVDQVKPKI 240
QY 241 ALLKFDVKDPK 251
DB 241 ALLKFDVKDPK 251

RESULT 14

PCT-US92-09487-2
; Sequence 2, Application PC/TUS9209487
; GENERAL INFORMATION:
; APPLICANT: Bernhard, Susan L.

;; APPLICANT: Better, Marc D.
;; APPLICANT: Carroll, Stephen F.
;; APPLICANT: Lane, Julie A.
;; APPLICANT: Lei, Shau-Ping
;; TITLE OF INVENTION: Materials Comprising and Methods of
;; TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins
;; NUMBER OF SEQUENCES: 101
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Marshhall, O'Toole, Gerstein, Murray &
;; ADDRESSEE: Bicknell,
;; STREET: Two First National Plaza, 20 South Clark
;; STREET: Street
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: USA
;; ZIP: 60603
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US92/09487
;; FILING DATE: 19921104
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/901,707
;; FILING DATE: 19-JUN-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/787,567
;; FILING DATE: 04-NOV-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Noland, Greta E.
;; REGISTRATION NUMBER: 35302
;; REFERENCE/DOCKET NUMBER: 31133
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (312) 346-5750
;; TELEFAX: (312) 984-9740
;; TELEX: 25-3856
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 251 amino acids
;; TYPE: AMINO ACID
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; PCT-US92-09487-2

Query Match 99.8%; Score 1284; DB 4; Length 251;
Best Local Similarity 99.6%; Pred. No. 2.5e-124;
Matches 250; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLDTSFSTKGATYTYVNFNLRLVKLPKGNHGIPLLRKKDDPGKCFVLVALSNDN 60
DB 1 GLDTSFSTKGATYTYVNFNLRLVKLPKGNHGIPLLRKKDDPGKCFVLVALSNDN 60
QY 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
DB 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKL DENAIDNYKPTIEASLLVVIQWSEAAARFTFIEQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKL DENAIDNYKPTIEASLLVVIQWSEAAARFTFIEQIRNN 180
QY 181 FOQIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEERANGKYYVTAVDQVKPKI 240
DB 181 FOQIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEERANGKYYVTAVDQVKPKI 240
QY 241 ALLKFDVKDPK 251
DB 241 ALLKFDVKDPK 251

RESULT 15

US-08-621-803-259
; Sequence 259, Application US/08621803
; Patent No. 5851802
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; TITLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/621,803
; FILING DATE: 22-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 259:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 293 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-621-803-259

Query Match 99.8%; Score 1284; DB 1; Length 293;
Best Local Similarity 99.6%; Pred. No. 3.1e-124; Mismatches 0; Indels 0; Gaps 0;
Matches 250; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLDTSFSTKGATYITYNFLNELRVKLPENSHGIPLLRKKDDPGKCFVLVALSNDN 60
DB 23 GLDTSFSTKGATYITYNFLNELRVKLPENSHGIPLLRKKDDPGKCFVLVALSNDN 82
QY 61 QQLABIAIDVTSVYVGVQVRNRSYFFKDDAPDAAYEGLPKNTIKTRLHFGSGYPSLEGEK 120
DB 83 QQLABIAIDVTSVYVGVQVRNRSYFFKDDAPDAAYEGLPKNTIKTRLHFGSGYPSLEGEK 142
QY 121 AYRETTDLGIEPLRIGIKL DENAIDNYPTEIASLLVVIOMVSEAAFTFIENQIRNN 180
DB 143 AYRETTDLGIEPLRIGIKL DENAIDNYPTEIASLLVVIOMVSEAAFTFIENQIRNN 202
QY 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240
DB 203 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 262
QY 241 ALLKFPVDKDPK 251
DB 263 ALLKFPVDKDPK 273

Search completed: February 10, 2006, 10:15:57
Job time : 51.0148 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 10, 2006, 10:37:59 ; Search time 163.937 Seconds
(without alignments)
639.727 Million cell updates/sec

Title: US-10-717-243-2
Perfect score: 1287
Sequence: 1 GLDTSFSTKGATYYVNF.....AVDQVKPALLKFVDKDPK 251

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1287	100.0	251	3	US-09-765-527-247
2	1287	100.0	251	4	US-10-127-890-2
3	1287	100.0	251	5	US-10-717-243-2
4	1287	100.0	316	4	US-10-074-596-1
5	1287	100.0	498	5	US-10-964-195-13
6	1287	100.0	507	4	US-10-074-596-11
7	1284	99.8	293	3	US-09-765-527-259
8	1284	99.8	309	3	US-09-765-527-253
9	1284	99.8	332	3	US-09-765-527-251
10	1283	99.7	751	6	US-11-084-080-26
11	1282	99.6	251	4	US-10-127-890-108
12	1282	99.6	251	5	US-10-717-243-108
13	1279	99.4	251	4	US-10-127-890-103
14	1279	99.4	251	4	US-10-127-890-104
15	1279	99.4	251	4	US-10-127-890-105
16	1279	99.4	251	4	US-10-127-890-106
17	1279	99.4	251	4	US-10-127-890-109
18	1279	99.4	251	5	US-10-717-243-103
19	1279	99.4	251	5	US-10-717-243-104
20	1279	99.4	251	5	US-10-717-243-105
21	1279	99.4	251	5	US-10-717-243-106
22	1279	99.4	251	5	US-10-717-243-109
23	1278	99.3	251	4	US-10-127-890-99
24	1278	99.3	251	4	US-10-127-890-100
25	1278	99.3	251	4	US-10-127-890-102
26	1278	99.3	251	4	US-10-127-890-107
27	1278	99.3	251	5	US-10-717-243-99

28	1278	99.3	251	5	US-10-717-243-100	Sequence 100, App
29	1278	99.3	251	5	US-10-717-243-102	Sequence 102, App
30	1278	99.3	251	5	US-10-717-243-107	Sequence 107, App
31	1269	98.6	251	4	US-10-127-890-101	Sequence 101, App
32	1269	98.6	251	5	US-10-717-243-101	Sequence 101, App
33	1261	98.0	251	4	US-10-127-890-110	Sequence 110, App
34	1261	98.0	251	5	US-10-717-243-110	Sequence 110, App
35	1252	97.3	251	4	US-10-127-890-111	Sequence 111, App
36	1252	97.3	251	5	US-10-717-243-111	Sequence 111, App
37	1219.5	94.8	513	5	US-10-926-731A-12	Sequence 12, Appl
38	1208	93.9	506	5	US-10-964-195-11	Sequence 11, Appl
39	346	26.9	263	4	US-10-127-890-4	Sequence 4, Appl
40	343	26.7	267	4	US-10-282-935-1	Sequence 1, Appl
41	343	26.7	267	4	US-10-127-890-1	Sequence 1, Appl
42	343	26.7	267	4	US-10-440-796-1	Sequence 1, Appl
43	343	26.7	267	5	US-10-717-243-1	Sequence 1, Appl
44	343	26.7	267	5	US-10-083-336A-1	Sequence 1, Appl
45	343	26.7	576	4	US-10-083-336A-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-765-527-247
; Sequence 247, Application US/09765527
; Patent No. US20020006638A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of Fusion Proteins and BPI-Derived Peptides
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,527
; FILING DATE: 18-Jan-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/621,803
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 247:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 247:
US-09-765-527-247

Query Match: 100.0%; Score 1287; DB 3; Length 251;
Best Local Similarity 100.0%; Pred. No. 6.3e-117; Indels 0; Gaps 0;
Matches 251; Conservative 0; Mismatches 0;
1 GLDTSFSTKGATYYVNFLELRVLPKPGNSHGIPLLRKKDDPGKCFVLVSLNDN 60
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Db 1 GLDVTSTGKATYTYVNFNLRLVKLPGNSHGIPLLRKKDDPGKCFVLVALSNDN 60
QY 61 GQLAEIADVTSVVVGQVNRNSYFFKADAPDAAYEGLFKNTIKTRLHFGSGSYPSLEGEK 120
Db 61 GQLAEIADVTSVVVGQVNRNSYFFKADAPDAAYEGLFKNTIKTRLHFGSGSYPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENADINYPKTEIASLLVVIOMVSEAAARFTFIENQIRNN 180
Db 121 AYRETTDLGIEPLRIGIKKLDENADINYPKTEIASLLVVIOMVSEAAARFTFIENQIRNN 180
QY 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEERANGKYYVTAVDQVKPKI 240
Db 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEERANGKYYVTAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
Db 241 ALLKFVDKDPK 251

RESULT 2

US-10-127-890-2
; Sequence 2, Application US/10127890
; Publication No. US20030166196A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Carroll, Stephen F.
; Studnika, Gary M.

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
Proteins

NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/127,890
FILING DATE: 23-Apr-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:

NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-127-890-2

Query Match 100.0%; Score 1287; DB 4; Length 251;
Best Local Similarity 100.0%; Pred. No. 6.3e-117;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLDVTSTGKATYTYVNFNLRLVKLPGNSHGIPLLRKKDDPGKCFVLVALSNDN 60
Db 1 GLDVTSTGKATYTYVNFNLRLVKLPGNSHGIPLLRKKDDPGKCFVLVALSNDN 60
QY 61 GQLAEIADVTSVVVGQVNRNSYFFKADAPDAAYEGLFKNTIKTRLHFGSGSYPSLEGEK 120
Db 61 GQLAEIADVTSVVVGQVNRNSYFFKADAPDAAYEGLFKNTIKTRLHFGSGSYPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENADINYPKTEIASLLVVIOMVSEAAARFTFIENQIRNN 180
Db 121 AYRETTDLGIEPLRIGIKKLDENADINYPKTEIASLLVVIOMVSEAAARFTFIENQIRNN 180
QY 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEERANGKYYVTAVDQVKPKI 240
Db 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEERANGKYYVTAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
Db 241 ALLKFVDKDPK 251

RESULT 3

US-10-717-243-2
; Sequence 2, Application US/10717243
; Publication No. US20050054835A1
; GENERAL INFORMATION:

APPLICANT: Better, Marc D.
Carroll, Stephen F.
Studnika, Gary M.

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
Proteins

NUMBER OF SEQUENCES: 169

CORRESPONDENCE ADDRESS:

ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/717,243
FILING DATE: 18-Nov-2003
CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/839,765
FILING DATE: 15-APR-1997
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:

NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
TELECOMMUNICATION INFORMATION:


```
;
; TELEPHONE: 312/707-8899
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-717-243-2

Query Match 100.0%; Score 1287; DB 5; Length 251;
Best Local Similarity 100.0%; Pred. No. 6.3e-117;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLDVSFSTKGTATITVYVFNELRVKLPKGNHGIPLLRKCCDDPKCFVLVSLNDN 60
DB 1 GLDVSFSTKGTATITVYVFNELRVKLPKGNHGIPLLRKCCDDPKCFVLVSLNDN 60
QY 61 QGLAEIAIDVTSVYVVGQVNRNSYFFKDAADAAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
DB 61 QGLAEIAIDVTSVYVVGQVNRNSYFFKDAADAAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTIEASSLLVVIQMVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTIEASSLLVVIQMVSEAAARFTFIENQIRNN 180
QY 181 FOORIRPANNTISLENKWGKLSFOIRTSGANGMFSEAVELERANGKYYVTAVDQVKPKI 240
DB 181 FOORIRPANNTISLENKWGKLSFOIRTSGANGMFSEAVELERANGKYYVTAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 4
US-10-074-596-1
; Sequence 1, Application US/10074596
; Publication No. US20030176331A1
; GENERAL INFORMATION:
; APPLICANT: ROSENBLUM, MICHAEL G.
; APPLICANT: CHEUNG, LAWRENCE
; TITLE OF INVENTION: MODIFIED PROTEINS, DESIGNER TOXINS, AND METHODS OF
; FILE REFERENCE: CLFR:007US
; CURRENT APPLICATION NUMBER: US/10/074,596
; CURRENT FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: 60/268,402
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Gelonium multiflorum
US-10-074-596-1

Query Match 100.0%; Score 1287; DB 4; Length 316;
Best Local Similarity 100.0%; Pred. No. 8.6e-117;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLDVSFSTKGTATITVYVFNELRVKLPKGNHGIPLLRKCCDDPKCFVLVSLNDN 60
DB 47 GLDVSFSTKGTATITVYVFNELRVKLPKGNHGIPLLRKCCDDPKCFVLVSLNDN 106
QY 61 QGLAEIAIDVTSVYVVGQVNRNSYFFKDAADAAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
DB 107 QGLAEIAIDVTSVYVVGQVNRNSYFFKDAADAAAYEGLFKNTIKTRLHFGGSYPSLEGEK 166
QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTIEASSLLVVIQMVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTIEASSLLVVIQMVSEAAARFTFIENQIRNN 180

;
; TELEPHONE: 312/707-8899
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-717-243-2

Query Match 100.0%; Score 1287; DB 5; Length 251;
Best Local Similarity 100.0%; Pred. No. 6.3e-117;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLDVSFSTKGTATITVYVFNELRVKLPKGNHGIPLLRKCCDDPKCFVLVSLNDN 60
DB 1 GLDVSFSTKGTATITVYVFNELRVKLPKGNHGIPLLRKCCDDPKCFVLVSLNDN 60
QY 61 QGLAEIAIDVTSVYVVGQVNRNSYFFKDAADAAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
DB 61 QGLAEIAIDVTSVYVVGQVNRNSYFFKDAADAAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTIEASSLLVVIQMVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTIEASSLLVVIQMVSEAAARFTFIENQIRNN 180
QY 181 FOORIRPANNTISLENKWGKLSFOIRTSGANGMFSEAVELERANGKYYVTAVDQVKPKI 240
DB 181 FOORIRPANNTISLENKWGKLSFOIRTSGANGMFSEAVELERANGKYYVTAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 5
US-10-964-195-13
; Sequence 13, Application US/10964195
; Publication No. US20050163774A1
; GENERAL INFORMATION:
; APPLICANT: Rosenblum et al.
; TITLE OF INVENTION: Immunotoxins Directed Against c-erbB-2 (HER-2/Neu)
; FILE REFERENCE: D5425CIP2
; CURRENT APPLICATION NUMBER: US/10/964,195
; CURRENT FILING DATE: 2004-10-13
; PRIOR APPLICATION NUMBER: US/09/320,156
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: 08/404,499
; PRIOR FILING DATE: 1995-03-17
; NUMBER OF SEQ ID NOS: 14
; SEQ ID NO 13
; LENGTH: 498
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Polypeptide encoded by the scFv23-gelonin immunotoxin
US-10-964-195-13

Query Match 100.0%; Score 1287; DB 5; Length 498;
Best Local Similarity 100.0%; Pred. No. 1.6e-116;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLDVSFSTKGTATITVYVFNELRVKLPKGNHGIPLLRKCCDDPKCFVLVSLNDN 60
DB 247 GLDVSFSTKGTATITVYVFNELRVKLPKGNHGIPLLRKCCDDPKCFVLVSLNDN 306
QY 61 QGLAEIAIDVTSVYVVGQVNRNSYFFKDAADAAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
DB 307 QGLAEIAIDVTSVYVVGQVNRNSYFFKDAADAAAYEGLFKNTIKTRLHFGGSYPSLEGEK 366
QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTIEASSLLVVIQMVSEAAARFTFIENQIRNN 180
DB 367 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTIEASSLLVVIQMVSEAAARFTFIENQIRNN 426
QY 181 FOORIRPANNTISLENKWGKLSFOIRTSGANGMFSEAVELERANGKYYVTAVDQVKPKI 240
DB 427 FOORIRPANNTISLENKWGKLSFOIRTSGANGMFSEAVELERANGKYYVTAVDQVKPKI 486
QY 241 ALLKFVDKDPK 251
DB 487 ALLKFVDKDPK 497

RESULT 6
US-10-074-596-11
; Sequence 11, Application US/10074596
; Publication No. US20030176331A1
; GENERAL INFORMATION:
; APPLICANT: ROSENBLUM, MICHAEL G.
; APPLICANT: CHEUNG, LAWRENCE
; TITLE OF INVENTION: MODIFIED PROTEINS, DESIGNER TOXINS, AND METHODS OF
; FILE REFERENCE: CLFR:007US
; CURRENT APPLICATION NUMBER: US/10/074,596
; CURRENT FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: 60/268,402
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SEQUENCE DESCRIPTION: SEQ ID NO: 253;
US-09-765-527-253

Query Match 99.8%; Score 1284; DB 3; Length 309;
Best Local Similarity 99.6%; Pred. No. 1.6e-116;
Matches 250; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLDTSFSTKGATYITVNFNLRLVKLPKGNHSHGIPLLRKKDDPKGCFVLVALSDN 60
Db GLDTSFSTKGATYITVNFNLRLVKLPKGNHSHGIPLLRKKDDPKGCFVLVALSDN 82

Qy 61 GOLAEIAIDVTSVYVVGQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGGYSYPSLEGEK 120
Db GOLAEIAIDVTSVYVVGQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGGYSYPSLEGEK 142

Qy 121 AYRETTDLGIEPLRIGIKKLDENADNPKTEIASLLVVIQVSEARFTFIENQIRNN 180
Db AYRETTDLGIEPLRIGIKKLDENADNPKTEIASLLVVIQVSEARFTFIENQIRNN 202

Qy 181 FQOIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
Db FQOIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 262

Qy 241 ALLKFPVDKDPK 251
Db ALLKFPVDKDPK 273

RESULT 9
US-09-765-527-251
; Sequence 251, Application US/09765527
; Patent No. US2002006638A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/09/765,527
; FILING DATE: 18-Jan-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/621,803
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 251:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 332 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 251:
US-09-765-527-251

Query Match 99.8%; Score 1284; DB 3; Length 332;

Best Local Similarity 99.6%; Pred. No. 1.8e-116;
Matches 250; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLDTSFSTKGATYITVNFNLRLVKLPKGNHSHGIPLLRKKDDPKGCFVLVALSDN 60
Db GLDTSFSTKGATYITVNFNLRLVKLPKGNHSHGIPLLRKKDDPKGCFVLVALSDN 82

Qy 61 GOLAEIAIDVTSVYVVGQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGGYSYPSLEGEK 120
Db GOLAEIAIDVTSVYVVGQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGGYSYPSLEGEK 142

Qy 121 AYRETTDLGIEPLRIGIKKLDENADNPKTEIASLLVVIQVSEARFTFIENQIRNN 180
Db AYRETTDLGIEPLRIGIKKLDENADNPKTEIASLLVVIQVSEARFTFIENQIRNN 202

Qy 181 FQOIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
Db FQOIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 262

Qy 241 ALLKFPVDKDPK 251
Db ALLKFPVDKDPK 273

RESULT 10
US-11-084-080-26
; Sequence 26, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis J.
; APPLICANT: HELLENDORF, Koen
; APPLICANT: CIZEAU, Jeannick
; APPLICANT: MACDONALD, Glen Christopher
; APPLICANT: ENTWISTLE, Joycelyn
; APPLICANT: BOSCH, Denis Georges
; APPLICANT: GLOVER, Nicholas Ronald
; TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND USES
; FILE REFERENCE: 10241-44
; CURRENT APPLICATION NUMBER: US/11/084,080
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US 60/554,580
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/630,571
; PRIOR FILING DATE: 2004-11-26
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 26
; LENGTH: 751
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VB6-845-gelonin
US-11-084-080-26

Query Match 99.7%; Score 1283; DB 6; Length 751;
Best Local Similarity 99.6%; Pred. No. 7e-116;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLDTSFSTKGATYITVNFNLRLVKLPKGNHSHGIPLLRKKDDPKGCFVLVALSDN 60
Db GLDTSFSTKGATYITVNFNLRLVKLPKGNHSHGIPLLRKKDDPKGCFVLVALSDN 313

Qy 61 GOLAEIAIDVTSVYVVGQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGGYSYPSLEGEK 120
Db GOLAEIAIDVTSVYVVGQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGGYSYPSLEGEK 373

Qy 121 AYRETTDLGIEPLRIGIKKLDENADNPKTEIASLLVVIQVSEARFTFIENQIRNN 180
Db AYRETTDLGIEPLRIGIKKLDENADNPKTEIASLLVVIQVSEARFTFIENQIRNN 433

Qy 181 FQOIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240

Query Match 99.6%; Score 1282; DB 5; Length 251;
Best Local Similarity 99.6%; Pred. No. 1.9e-116;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLDVSFSTKGATITTYVFNFLNLRVVKLPKPGNSHGIPLLRKKDDPKCFVLVALSNDN 60
DB 1 GLDVSFSTKGATITTYVFNFLNLRVVKLPKPGNSHGIPLLRKKDDPKCFVLVALSNDN 60

QY 61 GOLAEIADVTSVYVVGQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGSGYSLEGEK 120
DB 61 GOLAEIADVTSVYVVGQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGSGYSLEGEK 120

QY 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTETIASLLVWIQVSEAAARFTFIENQIERN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTETIASLLVWIQVSEAAARFTFIENQIERN 180

QY 181 FOQIRPANNTISLENKWKLSFOIRTSANGMFMSEAVELERANGKYYVTVAVDQVKPKI 240
DB 181 FOQIRPANNTISLENKWKLSFOIRTSANGMFMSEAVELERANGKYYVTVAVDQVKPKI 240

QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 13
US-10-127-890-103
; Sequence 103, Application US/10127890
; Publication No. US20030166196A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Carroll, Stephen F.
; Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating

Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/127,890
; FILING DATE: 23-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155

TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 103:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 103:
US-10-127-890-103

Query Match 99.4%; Score 1279; DB 4; Length 251;
Best Local Similarity 99.6%; Pred. No. 3.8e-116;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLDVSFSTKGATITTYVFNFLNLRVVKLPKPGNSHGIPLLRKKDDPKCFVLVALSNDN 60
DB 1 GLDVSFSTKGATITTYVFNFLNLRVVKLPKPGNSHGIPLLRKKDDPKCFVLVALSNDN 60

QY 61 GOLAEIADVTSVYVVGQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGSGYSLEGEK 120
DB 61 GOLAEIADVTSVYVVGQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGSGYSLEGEK 120

QY 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTETIASLLVWIQVSEAAARFTFIENQIERN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTETIASLLVWIQVSEAAARFTFIENQIERN 180

QY 181 FOQIRPANNTISLENKWKLSFOIRTSANGMFMSEAVELERANGKYYVTVAVDQVKPKI 240
DB 181 FOQIRPANNTISLENKWKLSFOIRTSANGMFMSEAVELERANGKYYVTVAVDQVKPKI 240

QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 14
US-10-127-890-104
; Sequence 104, Application US/10127890
; Publication No. US20030166196A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Carroll, Stephen F.
; Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/127,890
; FILING DATE: 23-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992

APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 104:
US-10-127-890-104

Query Match 99.4%; Score 1279; DB 4; Length 251;
Best Local Similarity 99.6%; Pred. No. 3.8e-116;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLDVSFSTKGATITTYVNFNLRLVKLPKPGNSHGIPLLRKKDDPGKCFVLVALSNDN 60
DB 1 GLDVSFSTKGATITTYVNFNLRLVKLPKPGNSHGIPLLRKKDDPGKCFVLVALSNDN 60

QY 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKADPAAAYEGLFKNTIKTRLHFGGSPSLEGEK 120
DB 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKADPAAAYEGLFKNTIKTRLHFGGSPSLEGEK 120

QY 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTKTEIASLLVVIQMVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTKTEIASLLVVIQMVSEAAARFTFIENQIRNN 180

QY 181 FQORIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240
DB 181 FQORIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240

QY 241 ALLKFDVDDPK 251
DB 241 ALLKFDVDDPK 251

RESULT 15
US-10-127-890-105
Sequence 105, Application US/10127890
Publication No. US20030166196A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
Carroll, Stephen F.
Studnicka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSER: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/127,890
FILING DATE: 23-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION NUMBER: US/08/646,360

FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 105:
US-10-127-890-105

Query Match 99.4%; Score 1279; DB 4; Length 251;
Best Local Similarity 99.6%; Pred. No. 3.8e-116;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLDVSFSTKGATITTYVNFNLRLVKLPKPGNSHGIPLLRKKDDPGKCFVLVALSNDN 60
DB 1 GLDVSFSTKGATITTYVNFNLRLVKLPKPGNSHGIPLLRKKDDPGKCFVLVALSNDN 60

QY 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKADPAAAYEGLFKNTIKTRLHFGGSPSLEGEK 120
DB 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKADPAAAYEGLFKNTIKTRLHFGGSPSLEGEK 120

QY 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTKTEIASLLVVIQMVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTKTEIASLLVVIQMVSEAAARFTFIENQIRNN 180

QY 181 FQORIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240
DB 181 FQORIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240

QY 241 ALLKFDVDDPK 251
DB 241 ALLKFDVDDPK 251

Search completed: February 10, 2006, 10:44:45
Job time : 164.937 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 10, 2006, 09:56:49 ; Search time 136.614 Seconds
(without alignments)
807.265 Million cell updates/sec

Title: US-10-717-243-2

Perfect score: 1287

Sequence: 1 GLDTSFSTKGATYYTNF.....AVDQVKPKIALKFKVDKPK 251

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq 21.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1287	100.0	251	2	AAR63903 Type I ri
2	1287	100.0	251	8	ADG63044 Gelonium
3	1287	100.0	316	5	ABG71551 G. multif
4	1287	100.0	498	9	AEB68722 scFv23-ge
5	1287	100.0	507	5	ABG71552 Murine sc
6	1284	99.8	293	2	Aaw29300 BPI pepti
7	1284	99.8	309	2	Aaw29303 BPI pepti
8	1284	99.8	332	2	Aaw29294 BPI pepti
9	1282	98.6	251	2	AAR63923 Type I RI
10	1279	99.4	251	2	AAR63921 Type I RI
11	1279	99.4	251	2	AAR63918 Type I RI
12	1279	99.4	251	2	AAR63920 Type I RI
13	1279	99.4	251	2	AAR63919 Type I RI
14	1279	99.4	251	2	AAR63924 Type I RI
15	1278	99.3	251	2	AAR63922 Type I RI
16	1278	99.3	251	2	AAR63917 Type I RI
17	1278	99.3	251	2	AAR63912 Type I RI
18	1275	99.1	251	2	AAR74177 Type I ri
19	1269	98.6	251	2	AAR37291 Plant typ
20	1269	98.6	251	2	AAR63914 Type I RI
21	1261	98.0	251	2	AAR63915 Type I RI
22	1252	97.3	251	2	AAR63916 Type I RI
23	1242.5	96.5	258	2	AAR22227 Gelonin t
24	1208	93.9	506	9	AEB68720 scFv23-ge

25	1176	91.4	235	2	AAR63913	Aar63913 Type I RI
26	346	26.9	263	2	AAR63905	Aar63905 Type I ri
27	346	26.9	263	2	AAR74179	Aar74179 Type I ri
28	346	26.9	263	8	ADG63043	Adg63043 Momordica
29	344	26.7	565	1	AAP50166	Aap50166 Sequence
30	344	26.7	565	4	AAG78300	Castor be
31	344	26.7	574	1	AAP70325	Aap70325 Sequence
32	343	26.7	267	2	AAR30722	Aar30722 Ricin A f
33	343	26.7	267	2	AAR37290	Ricin A c
34	343	26.7	267	2	AAR63902	Ricin A-c
35	343	26.7	267	3	AB19265	Amino aci
36	343	26.7	267	7	ADC24288	Ricin tox
37	343	26.7	268	2	AAR39570	Sequence
38	343	26.7	290	2	Aaw21699	Aaw21699 Ricin A-c
39	343	26.7	290	2	Aaw25136	Ricin A-c
40	343	26.7	332	1	AAP70097	Ricin A-
41	343	26.7	332	1	AAP70838	Sequence
42	343	26.7	332	1	AAP95639	Ricin A e
43	343	26.7	554	2	AAR70827	Anti-cata
44	343	26.7	562	1	AAP90079	Aap90079 Ricin D.
45	343	26.7	565	4	AAG78304	Modified

ALIGNMENTS

RESULT 1

AAR63903

ID AAR63903 standard; protein; 251 AA.

AC AAR63903;

DT 25-MAR-2003 (revised)

DT 27-JUL-1995 (first entry)

XX Type I ribosome-inactivating protein gelonin.

XX Type I ribosome-inactivating proteins; RIPs; gelonin;
XX cytotoxic therapeutic agents; autoimmune disease; cancer;
XX graft-versus-host disease.

OS Gelonium multiflorum.

XX WO9426910-A1.

PD 24-NOV-1994.

XX 12-MAY-1994; 94WO-US005348.

PR 12-MAY-1993; 93US-00064691.

XX (XOMA) XOMA CORP.

PI Better MD, Carroll SF, Studnicka GW;

XX WPI; 1995-006804/01.

DR N-PSDB; AAQ75532.

XX Polynucleotide(s) encoding type I ribosome-inactivating proteins - which
XX are suitable for use as components of cytotoxic therapeutic agents.
XX Example 1; Fig 1; 221pp; English.

CC AAQ75532 encodes AAR63903 type I ribosome-inactivating protein (RIP)
CC gelonin, one of the nine RIPs described in AAR63903-Re3911. RIPs are key
CC components of cytotoxic therapeutic agents (CTAs), which include gene
CC fusion products and immunoconjugates. CTAs may be used to selectively
CC eliminate any cell type to which a RIP component is targeted, by the
CC specific binding capacity of the second component of the agent. They can
CC be used in the treatment of diseases where the elimination of a
CC particular cell type is desired, such as autoimmune disease, cancer and
CC graft-versus-host disease. (Updated on 25-MAR-2003 to correct PN field.)


```

SQ Sequence 251 AA;
Query Match 100.0%; Score 1287; DB 2; Length 251;
Best Local Similarity 100.0%; Pred. No. 1.8e-125;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLDTSFSTKGATITTYVNFNLRLVKLPKPGNSHGIPLLRKKCDPDKCFVLVALSNDN 60
DB 1 GLDTSFSTKGATITTYVNFNLRLVKLPKPGNSHGIPLLRKKCDPDKCFVLVALSNDN 60

QY 61 QGLAEIAIDVTSVYVGVQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGSGYPSLEGEK 120
DB 61 QGLAEIAIDVTSVYVGVQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGSGYPSLEGEK 120

QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTBIASSLLVVIQWSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTBIASSLLVVIQWSEAAARFTFIENQIRNN 180

QY 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEERANGKYYVTAVDQVKPKI 240
DB 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEERANGKYYVTAVDQVKPKI 240

QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 2
ADG63044
ID ADG63044 standard; protein; 251 AA.
XX AC ADG63044;
XX DT 11-MAR-2004 (first entry)
XX DE Gelonium anti-HIV protein 31kDa (GAP31).
XX KW anti-HIV; cytostatic; peptide therapy; anti-tumour; antiviral; MAP30;
XX KW GAP31; HIV; tumour; gelonium anti-HIV protein 31kDa.
XX OS Gelonium multiflorum.
XX PN US6652861-B1.
XX PD 25-NOV-2003.
XX PF 25-AUG-2000; 2000US-00645603.
XX PR 26-AUG-1999; 99US-0150885P.
XX PA (UYN) ) UNIV NEW YORK STATE.
XX PI Lee-Huang S;
XX DR WPI; 2004-050519/05.
XX PT New MAP30 or GAP31 peptides or polypeptides having an anti-tumor and
PT PT antiviral activity, useful for treating human immunodeficiency virus
PT PT infection or tumor.
XX PS Example 1; SEQ ID NO 2; 22pp; English.
XX CC The invention describes an isolated peptide or polypeptide having an anti-
CC CC -tumour and antiviral activity. Also described is a composition
CC CC comprising the isolated peptide or polypeptide, and a carrier, excipient
CC CC or auxiliary agent. Specifically claimed are MAP30 or GAP31 peptides or
CC CC polypeptides. The peptide or polypeptide is useful for treating HIV
CC CC infection, and tumour. This is the amino acid sequence of Gelonium anti-
CC CC HIV protein 30kDa (MAP30).
SQ Sequence 251 AA;
Query Match 100.0%; Score 1287; DB 8; Length 251;
Best Local Similarity 100.0%; Pred. No. 1.8e-125;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLDTSFSTKGATITTYVNFNLRLVKLPKPGNSHGIPLLRKKCDPDKCFVLVALSNDN 60
DB 1 GLDTSFSTKGATITTYVNFNLRLVKLPKPGNSHGIPLLRKKCDPDKCFVLVALSNDN 60

QY 61 QGLAEIAIDVTSVYVGVQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGSGYPSLEGEK 120
DB 61 QGLAEIAIDVTSVYVGVQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGSGYPSLEGEK 120

QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTBIASSLLVVIQWSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTBIASSLLVVIQWSEAAARFTFIENQIRNN 180

QY 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEERANGKYYVTAVDQVKPKI 240
DB 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEERANGKYYVTAVDQVKPKI 240

QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 3
ABG71551
ID ABG71551 standard; protein; 316 AA.
XX AC ABG71551;
XX DT 08-JAN-2003 (first entry)
XX DE G. multiflorum recombinant gelonin (rGel) toxin.
XX KW Modified protein; reduced antigenicity; modified toxin; gelonin;
XX KW designer toxin; immunotoxin; proteinaceous compound; cancer;
XX KW microbial pathogenesis; acquired immunodeficiency syndrome; AIDS;
XX KW autoimmune disease; hyperproliferative disorder; leukaemia; arthritis;
XX KW inflammatory disease; cardiovascular disease; diabetes;
XX KW pathogenic disease; cytostatic; antiarthritic; antiinflammatory;
XX KW cardiant; antidiabetic; virucide; protozoacide; fungicide; antibacterial;
XX KW recombinant gelonin; rGel.
XX OS Gelonium multiflorum.
XX PN WO200269886-A2.
XX PD 12-SEP-2002.
XX PF 12-FEB-2002; 2002WO-US004195.
XX PR 12-FEB-2001; 2001US-0268402P.
XX PA (RERE-) RES DEV FOUND.
XX PI Rosenblum MG, Cheung L;
XX DR WPI; 2002-750431/81.
XX DR N-PSDB; ABS56021.
XX PT Generating a modified protein with reduced antigenicity for treating
PT PT cancer, AIDS, autoimmune diseases, comprises identifying a protein region
PT PT antigenic in the first subject using antiserum from either the first or a
PT PT second subject.
XX PS Claim 63; Page 169-170; 176pp; English.
XX CC The present invention relates to a method of generating a modified
CC CC protein with reduced antigenicity while maintaining its biological
CC CC activity. The method comprises identifying a region of the protein that
CC CC is antigenic in a first subject using antiserum from either the first
CC CC subject or a second subject of the same species as the first subject. In
CC CC particular the invention discloses modified toxin compounds, for example

```


CC gelonin toxin derived from Gelonium multiflorum, that are truncated
 CC and/or possess reduced antigenicity. Such designer toxins have
 CC therapeutic, diagnostic, and preventative benefits, particularly as
 CC immunotoxins. The method of the invention is useful for generating
 CC proteinaceous compounds with less antigenicity. The immunotoxin and
 CC gelonin toxin are useful for treating cancer, e.g. prostate, lung, brain,
 CC skin, liver, breast, lymphoid, stomach, testicular, ovarian, pancreatic,
 CC bone, bone marrow, head and neck, cervical, oesophagus, eye, gall
 CC bladder, kidney, adrenal glands, heart, colon, or blood cancer. The
 CC compositions of the invention are also useful for treating microbial
 CC pathogenesis, acquired immunodeficiency syndrome (AIDS), autoimmune
 CC diseases, hyperproliferative disorders including cancer, leukemias,
 CC arthritis, inflammatory diseases, cardiovascular diseases, pathogenic
 CC diseases, and diabetes. The method provides less antigenic proteins,
 CC peptides and polypeptides, which are more effective than prior art. The
 CC present sequence represents G. multiflorum recombinant gelonin (rGel)
 XX
 XX Sequence 316 AA;

Query Match 100.0%; Score 1287; DB 5; Length 316;
 Best Local Similarity 100.0%; Pred. No. 2.5e-125;
 Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLDTVSFSTKGATITTYVNFNLRLVKLPKGNHSHGIPLLRKKCDPDKCFVLVALSNDN 60
 DB 47 GLDTVSFSTKGATITTYVNFNLRLVKLPKGNHSHGIPLLRKKCDPDKCFVLVALSNDN 106

QY 61 GQLAEIAIDVTSVVGVQVRNRSYFFKADPAAYEGLPKNTIKTRLHFGSGSYPSLEGK 120
 DB 107 GQLAEIAIDVTSVVGVQVRNRSYFFKADPAAYEGLPKNTIKTRLHFGSGSYPSLEGK 166

QY 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTIASLLVVIQVSEAAARFTFIENQIRNN 180
 DB 167 AYRETTDLGIEPLRIGIKKLDENADNYKPTIASLLVVIQVSEAAARFTFIENQIRNN 226

QY 181 FQQRIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240
 DB 227 FQQRIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 286

QY 241 ALLKPVDDKPK 251
 DB 287 ALLKPVDDKPK 297

RESULT 4
 ID AEB68722 standard; protein; 498 AA.
 XX
 AC AEB68722;
 DT 06-OCT-2005 (first entry)
 XX
 DE scFv23-gelonin immunotoxin amino acid sequence SEQ ID NO:13.
 XX antibody engineering; c-erbB-2 protein; toxin; gelonin; cytostatic;
 KW immunotoxin; neoplasm.
 XX Synthetic.
 OS
 XX US2005163774-A1.
 PN
 PD 28-JUL-2005.
 XX
 PF 13-OCT-2004; 2004US-00964195.
 XX
 PR 10-APR-1992; 92US-00867728.
 PR 09-DEC-1993; 93US-00164638.
 PR 02-SEP-1994; 94US-00300082.
 PR 17-MAR-1995; 95US-00404499.
 PR 26-MAY-1999; 99US-00320156.
 XX
 XX (RERE-) RES DEV FOUND.

PI Rosenblum M, Shawver LK;
 XX WPI; 2005-561813/57.
 DR N-PSDB; AEB68721.
 XX
 PT New immunotoxins directed against c-erbB-2 related surface antigens,
 PT useful for treating neoplastic diseases, e.g. carcinoma or
 PT adenocarcinoma.
 XX
 PS Disclosure; SEQ ID NO 13; 60pp; English.
 XX
 CC The invention relates to a composition comprising a conjugate of an
 CC antibody exhibiting binding specificity for an extracellular epitope of c
 CC -erbB-2 protein and a plant derived toxin, where the toxin is
 CC pharmacologically effective against neoplastic cells and is selected from
 CC gelonin, full length recombinant gelonin, functional gelonin fragments or
 CC functional gelonin derivatives. Also described is a pharmaceutical
 CC composition comprising the composition above and a pharmaceutical
 CC vehicle. For treating neoplastic diseases, e.g. human mammary carcinomas,
 CC human ovarian carcinomas, lung carcinomas, gastric tumors, salivary gland
 CC adenocarcinomas, or colon adenocarcinomas. The present sequence
 CC represents a scFv23-gelonin amino acid sequence, which is used in an
 CC example from the present invention.

XX Sequence 498 AA;

Query Match 100.0%; Score 1287; DB 9; Length 498;
 Best Local Similarity 100.0%; Pred. No. 4.9e-125;
 Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLDTVSFSTKGATITTYVNFNLRLVKLPKGNHSHGIPLLRKKCDPDKCFVLVALSNDN 60
 DB 247 GLDTVSFSTKGATITTYVNFNLRLVKLPKGNHSHGIPLLRKKCDPDKCFVLVALSNDN 306

QY 61 GQLAEIAIDVTSVVGVQVRNRSYFFKADPAAYEGLPKNTIKTRLHFGSGSYPSLEGK 120
 DB 307 GQLAEIAIDVTSVVGVQVRNRSYFFKADPAAYEGLPKNTIKTRLHFGSGSYPSLEGK 366

QY 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTIASLLVVIQVSEAAARFTFIENQIRNN 180
 DB 367 AYRETTDLGIEPLRIGIKKLDENADNYKPTIASLLVVIQVSEAAARFTFIENQIRNN 426

QY 181 FQQRIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240
 DB 427 FQQRIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 486

QY 241 ALLKPVDDKPK 251
 DB 487 ALLKPVDDKPK 497

RESULT 5
 ID AEB71552 standard; protein; 507 AA.
 XX
 AC AEB71552;
 XX
 DT 08-JAN-2003 (first entry)
 XX
 DE Murine scfWME/L/G. multiflorum rGel fusion protein.

XX Modified protein; reduced antigenicity; modified toxin; gelonin;
 KW designer toxin; immunotoxin; proteinaceous compound; cancer;
 KW microbial pathogenesis; acquired immunodeficiency syndrome; AIDS;
 KW autoimmune disease; hyperproliferative disorder; leukemias; arthritis;
 KW inflammatory disease; cardiovascular disease; diabetes;
 KW pathogenic disease; cytostatic; antiarthritic; antiinflammatory;
 KW cardiant; antidiabetic; virucide; protozoacide; fungicide; antibacterial;
 KW murine; single-chain ZME-018 antibody; recombinant gelonin; rGel;
 KW scfWME/L/rGel; mutant; mutein.
 XX
 OS Mus sp.
 OS Gelonium multiflorum.

OS Synthetic.
OS Chimeric.
XX WO200269886-A2.
PD 12-SEP-2002.
XX
XX 12-FEB-2002; 2002WO-US004195.
XX
XX 12-FEB-2001; 2001US-0268402P.
XX
XX (RESE-) RES DEV FOUND.
XX
XX Rosenblum MG, Cheung L;
XX
XX WPI; 2002-750431/81.
XX N-PSDB; ABS56029.
XX
XX Generating a modified protein with reduced antigenicity for treating
XX cancer, AIDS, autoimmune diseases, comprises identifying a protein region
XX antigenic in the first subject using antiserum from either the first or a
XX second subject.
XX
XX Disclosure; Page 174-176; 176pp; English.
XX
XX The present invention relates to a method of generating a modified
XX protein with reduced antigenicity while maintaining its biological
XX activity. The method comprises identifying a region of the protein that
XX is antigenic in a first subject using antiserum from either the first
XX subject or a second subject of the same species as the first subject. In
XX particular the invention discloses modified toxin compounds, for example
XX gelonin toxin derived from Gelonium multiflorum, that are truncated
XX and/or possess reduced antigenicity. Such designer toxins have
XX immunotoxic, diagnostic, and preventative benefits, particularly as
XX proteinaceous compounds with less antigenicity. The immunotoxin and
XX gelonin toxin are useful for treating cancer, e.g. prostate, lung, brain,
XX skin, liver, breast, lymphoid, stomach, testicular, ovarian, pancreatic,
XX bone, bone marrow, head and neck, cervical, oesophagus, eye, gall
XX bladder, kidney, adrenal glands, heart, colon, or blood cancer. The
XX compositions of the invention are also useful for treating microbial
XX pathogenesis, acquired immunodeficiency syndrome (AIDS), autoimmu
XX diseases, hyperproliferative disorders including cancer, leukaemias,
XX arthritis, inflammatory diseases, cardiovascular diseases, pathogenic
XX diseases, and diabetes. The method provides less antigenic proteins,
XX peptides and polypeptides, which are more effective than prior art. The
XX present sequence represents murine single-chain ZM8-018 antibody/G.
XX multiflorum recombinant gelonin (rGel) (scfvWEL/rGel) fusion protein
XX
XX Sequence 507 AA;
XX
XX Query Match 100.0%; Score 1287; DB 5; Length 507;
XX Best Local Similarity 100.0%; Pred. No. 5, 1e-125;
XX Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 GLDVSFSTKGATITTYVNFNLRLVKLPENSHGIPLLRKKDDPGKCFVLVSLNDN 60
XX 257 GLDVSFSTKGATITTYVNFNLRLVKLPENSHGIPLLRKKDDPGKCFVLVSLNDN 316
XX
XX 61 GQLAEIAIDVTSVYVVGQVRNRSYFFKDAADAAEGLFKNTIKTRLHFGGSSPSLEGEK 120
XX 317 GQLAEIAIDVTSVYVVGQVRNRSYFFKDAADAAEGLFKNTIKTRLHFGGSSPSLEGEK 376
XX
XX 121 AVRETTDLGIEPLRIGIKKL DENAIDNYKPTETASSLLVVIQWSEAAFTFIENQIRNN 180
XX 377 AVRETTDLGIEPLRIGIKKL DENAIDNYKPTETASSLLVVIQWSEAAFTFIENQIRNN 436
XX
XX 181 FQQRIRPANNTISLENKWKLSFQIRTS GANGMFSEAVELERANGKYYVTAVDQVKPKI 240
XX 437 FQQRIRPANNTISLENKWKLSFQIRTS GANGMFSEAVELERANGKYYVTAVDQVKPKI 496
XX
XX 241 ALLKFVDKDPK 251
XX

Db 497 ALLKFVDKDPK 507
XX
XX RESULT 6
XX AAW29300
XX ID AAW29300 standard; protein; 293 AA.
XX
XX AC AAW29300;
XX
XX DT 20-APR-1998 (first entry)
XX
XX BPI peptide fusion protein PING3797 vector construct protein.
XX
XX Bactericidal/permeability increasing peptide; BPI; fusion protein;
XX bacterial infection; fungal infection; endotoxin; heparin; angiogenesis;
XX fungicidal; recombinant DNA; vector.
XX
XX Synthetic.
XX Pectobacterium carotovorum.
XX Homo sapiens.
XX Chimeric.
XX
XX PN WO9735009-A1.
XX
XX PD 25-SEP-1997.
XX
XX PF 18-MAR-1997; 97WO-US005287.
XX
XX PR 22-MAR-1996; 96US-00621803.
XX
XX PA (XOMA) XOMA CORP.
XX
XX Better MD;
XX
XX WPI; 1997-480215/44.
XX N-PSDB; AAT86336.
XX
XX Recombinant production of bactericidal/permeability increasing protein -
XX by expression as a fusion protein in microbial host cells, then cleaving
XX the BPI peptide from the carrier.
XX
XX Example 1; Page 160-161; 186pp; English.
XX
XX A new recombinant DNA vector construct has been developed which encodes a
XX fusion protein and is suitable for introduction into a bacterial host.
XX The vector comprises: (a) DNA encoding at least one cationic
XX bactericidal/permeability increasing peptide (BPI), (b) DNA encoding a
XX carrier protein, and (c) DNA encoding an amino acid (aa) cleavage site
XX located between (a) and (b). The present sequence represents the protein
XX from the PING3797 vector construct which codes for a BPI fusion protein.
XX The peptides have many uses including the treatment of bacterial and
XX fungal infections. BPI peptides also bind to endotoxins and heparin,
XX neutralising their effects. The peptides have further been shown to
XX inhibit angiogenesis (partly due to heparin-binding activity). The fusion
XX proteins have been found to be expressed in large amounts without
XX significant proteolysis, and in some cases are actually secreted from the
XX host cells. This allows the indirect production of anti-microbial BPI
XX peptides in microbial hosts
XX
XX Sequence 293 AA;
XX
XX Query Match 99.8%; Score 1284; DB 2; Length 293;
XX Best Local Similarity 99.6%; Pred. No. 4, 7e-125;
XX Matches 250; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 GLDVSFSTKGATITTYVNFNLRLVKLPENSHGIPLLRKKDDPGKCFVLVSLNDN 60
XX 23 GLDVSFSTKGATITTYVNFNLRLVKLPENSHGIPLLRKKDDPGKCFVLVSLNDN 82
XX
XX 61 GQLAEIAIDVTSVYVVGQVRNRSYFFKDAADAAEGLFKNTIKTRLHFGGSSPSLEGEK 120
XX 83 GQLAEIAIDVTSVYVVGQVRNRSYFFKDAADAAEGLFKNTIKTRLHFGGSSPSLEGEK 142

QY 121 AYRETTDLGIEPLRIGIKKLDNAIDNYKPTBIASSLLVVIQMVSEAAARFTFIENQIRNN 180
 Db 143 AYRETTDLGIEPLRIGIKKLDNAIDNYKPTBIASSLLVVIQMVSEAAARFTFIENQIRNN 202
 QY 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKCKYYVTVAVDQVKPKI 240
 Db 203 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKCKYYVTVAVDQVKPKI 262
 QY 241 ALLKFVDKDPK 251
 Db 263 ALLKFVDKDPK 273

RESULT 7
 AAW29303
 ID AAW29303 standard; protein; 309 AA.
 XX
 AC AAW29303;
 XX
 DT 20-APR-1998 (first entry)
 XX
 DE BPI peptide fusion protein PING3795 vector construct protein.
 XX
 KW Bactericidal/permeability increasing peptide; BPI; fusion protein;
 KW bacterial infection; fungal infection; endotoxin; heparin; angiogenesis;
 KW fungicidal; recombinant DNA; vector.
 XX
 OS Synthetic.
 OS Pectobacterium carotovorum.
 OS Homo sapiens.
 OS Chimeric.
 XX
 PN WO9735009-A1.
 XX
 PD 25-SEP-1997.
 XX
 PF 18-MAR-1997; 97WO-US005287.
 XX
 PR 22-MAR-1996; 96US-00621803.
 XX
 PA (XOMA) XOMA CORP.
 XX
 PI Better MD;
 XX
 DR WPI; 1997-480215/44.
 DR N-PSDB; AAT86341.
 XX
 PT Recombinant production of bactericidal/permeability increasing protein -
 PT by expression as a fusion protein in microbial host cells, then cleaving
 PT the BPI peptide from the carrier.
 XX
 PS Example 1; Page 152-153; 186pp; English.
 XX
 CC A new recombinant DNA vector construct has been developed which encodes a
 CC fusion protein and is suitable for introduction into a bacterial host.
 CC The vector comprises: (a) DNA encoding at least one cationic
 CC bactericidal/permeability increasing peptide (BPI), (b) DNA encoding a
 CC carrier protein, and (c) DNA encoding an amino acid (aa) cleavage site
 CC located between (a) and (b). The present sequence represents the protein
 CC from the PING3795 vector construct which codes for a BPI fusion protein.
 CC The peptides have many uses including the treatment of bacterial and
 CC fungal infections. BPI peptides also bind to endotoxins and heparin,
 CC neutralising their effects. The peptides have further been shown to
 CC inhibit angiogenesis (partly due to heparin-binding activity). The fusion
 CC proteins have been found to be expressed in large amounts without
 CC significant proteolysis, and in some cases are actually secreted from the
 CC host cells. This allows the indirect production of anti-microbial BPI
 CC peptides in microbial hosts
 SQ Sequence 309 AA;

Query Match 99.8%; Score 1284; DB 2; Length 309;
 Best Local Similarity 99.6%; Pred. No. 5.1e-125;

Matches 250; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GLDTSVSTKGTATITTYVNFNLRLRVKLKPSGNSHGIPLLRKKCDPDKCFVLVALSNDN 60
 Db 23 GLDTSVSTKGTATITTYVNFNLRLRVKLKPSGNSHGIPLLRKKCDPDKCFVLVALSNDN 82
 QY 61 GOLABIAIDVTSVTVGVQVRNRSYFFPKADAPDAAYEGLFKNTIKTRLHFGSGSYPSLEGEK 120
 Db 83 GOLABIAIDVTSVTVGVQVRNRSYFFPKADAPDAAYEGLFKNTIKTRLHFGSGSYPSLEGEK 142
 QY 121 AYRETTDLGIEPLRIGIKKLDNAIDNYKPTBIASSLLVVIQMVSEAAARFTFIENQIRNN 180
 Db 143 AYRETTDLGIEPLRIGIKKLDNAIDNYKPTBIASSLLVVIQMVSEAAARFTFIENQIRNN 202
 QY 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKCKYYVTVAVDQVKPKI 240
 Db 203 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKCKYYVTVAVDQVKPKI 262
 QY 241 ALLKFVDKDPK 251
 Db 263 ALLKFVDKDPK 273

RESULT 8
 AAW29294
 ID AAW29294 standard; protein; 332 AA.
 XX
 AC AAW29294;
 XX
 DT 20-APR-1998 (first entry)
 XX
 DE BPI peptide fusion protein PING3793 vector construct protein.
 XX
 KW Bactericidal/permeability increasing peptide; BPI; fusion protein;
 KW bacterial infection; fungal infection; endotoxin; heparin; angiogenesis;
 KW fungicidal; recombinant DNA; vector.
 XX
 OS Synthetic.
 OS Pectobacterium carotovorum.
 OS Homo sapiens.
 OS Chimeric.
 XX
 PN WO9735009-A1.
 XX
 PD 25-SEP-1997.
 XX
 PF 18-MAR-1997; 97WO-US005287.
 XX
 PR 22-MAR-1996; 96US-00621803.
 XX
 PA (XOMA) XOMA CORP.
 XX
 PI Better MD;
 XX
 DR WPI; 1997-480215/44.
 DR N-PSDB; AAT86332.
 XX
 PT Recombinant production of bactericidal/permeability increasing protein -
 PT by expression as a fusion protein in microbial host cells, then cleaving
 PT the BPI peptide from the carrier.
 XX
 PS Example 1; Page 148-150; 186pp; English.
 XX
 CC A new recombinant DNA vector construct has been developed which encodes a
 CC fusion protein and is suitable for introduction into a bacterial host.
 CC The vector comprises: (a) DNA encoding at least one cationic
 CC bactericidal/permeability increasing peptide (BPI), (b) DNA encoding a
 CC carrier protein, and (c) DNA encoding an amino acid (aa) cleavage site
 CC located between (a) and (b). The present sequence represents the protein
 CC from the PING3793 vector construct which codes for a BPI fusion protein.
 CC The peptides have many uses including the treatment of bacterial and
 CC fungal infections. BPI peptides also bind to endotoxins and heparin,
 CC neutralising their effects. The peptides have further been shown to

CC inhibit angiogenesis (partly due to heparin-binding activity). The fusion
 CC proteins have been found to be expressed in large amounts without
 CC significant proteolysis, and in some cases are actually secreted from the
 CC host cells. This allows the indirect production of anti-microbial BPI
 CC peptides in microbial hosts

XX
 SQ Sequence 332 AA;

Query Match 99.8%; Score 1284; DB 2; Length 332;
 Best Local Similarity 99.6%; Pred. No. 5.6e-125;
 Matches 250; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLDTSFSTKGATYYVNFNLRLVKLPKGNHSHGIPLLRKKCDPDKGCFVLVALSNDN 60
 DB 23 GLDTSFSTKGATYYVNFNLRLVKLPKGNHSHGIPLLRKKCDPDKGCFVLVALSNDN 82
 QY 61 GOLAEIAIDVTSVYVVGQVRNRSYFFKADPAAYEGLFKNTIKTRLHFGSGYPSLEGEK 120
 DB 83 GOLAEIAIDVTSVYVVGQVRNRSYFFKADPAAYEGLFKNTIKTRLHFGSGYPSLEGEK 142
 QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQWSEAAARFTFIENQIRNN 180
 DB 143 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQWSEAAARFTFIENQIRNN 202
 QY 181 FOQIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
 DB 203 FOQIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 262
 QY 241 ALLKFEVDKDPK 251
 DB 263 ALLKFEVDKDPK 273

RESULT 9

AAR63923
 ID AAR63923 standard; protein; 251 AA.

XX
 AC AAR63923;

XX
 DT 25-MAR-2003 (revised)
 DT 27-JUL-1995 (first entry)

XX
 DE Type I RIP gelonin analog Gel (C103).

XX
 KW Type I ribosome-inactivating proteins; RIPS; gelonin;
 KW cytotoxic therapeutic agents; autoimmune disease; cancer;
 KW graft-versus-host disease.

XX
 OS Gelonium multiflorum.

XX
 PN WO9426910-A1.

XX
 PD 24-NOV-1994.

XX
 PF 12-MAY-1994; 94WO-US005348.

XX
 PR 12-MAY-1993; 93US-00064691.

XX
 PA (XOMA) XOMA CORP.

XX
 PI Better MD, Carroll SF, Studnicka GM;

XX
 DR WPI; 1995-006804/01.

XX
 PT Polynucleotide(s) encoding type I ribosome-inactivating proteins - which
 PT are suitable for use as components of cytotoxic therapeutic agents.

XX
 PS Example 3; Page 187-188; 221pp; English.

XX
 CC AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating
 CC protein (RIP) gelonin, one of the nine RIPS described in AAR63903-R63911.
 CC RIPS are key components of cytotoxic therapeutic agents (CTAs), which
 CC include gene fusion products and immunoconjugates. CTAs may be used to

CC selectively eliminate any cell type to which a RIP component is
 CC targeted, by the specific binding capacity of the second component of
 CC the agent. They can be used in the treatment of diseases where the
 CC elimination of a particular cell type is desired, such as autoimmune
 CC disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to
 CC correct PN field.)

XX
 SQ Sequence 251 AA;

Query Match 99.6%; Score 1282; DB 2; Length 251;
 Best Local Similarity 99.6%; Pred. No. 6.1e-125;
 Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLDTSFSTKGATYYVNFNLRLVKLPKGNHSHGIPLLRKKCDPDKGCFVLVALSNDN 60
 DB 1 GLDTSFSTKGATYYVNFNLRLVKLPKGNHSHGIPLLRKKCDPDKGCFVLVALSNDN 60
 QY 61 GOLAEIAIDVTSVYVVGQVRNRSYFFKADPAAYEGLFKNTIKTRLHFGSGYPSLEGEK 120
 DB 61 GOLAEIAIDVTSVYVVGQVRNRSYFFKADPAAYEGLFKNTIKTRLHFGSGYPSLEGEK 120
 QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQWSEAAARFTFIENQIRNN 180
 DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQWSEAAARFTFIENQIRNN 180
 QY 181 FOQIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
 DB 181 FOQIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
 QY 241 ALLKFEVDKDPK 251
 DB 241 ALLKFEVDKDPK 251

RESULT 10

AAR63921
 ID AAR63921 standard; protein; 251 AA.

XX
 AC AAR63921;

XX
 DT 25-MAR-2003 (revised)
 DT 27-JUL-1995 (first entry)

XX
 DE Type I RIP gelonin analog Gel (C10).

XX
 KW Type I ribosome-inactivating proteins; RIPS; gelonin;
 KW cytotoxic therapeutic agents; autoimmune disease; cancer;
 KW graft-versus-host disease.

XX
 OS Gelonium multiflorum.

XX
 PN WO9426910-A1.

XX
 PD 24-NOV-1994.

XX
 PF 12-MAY-1994; 94WO-US005348.

XX
 PR 12-MAY-1993; 93US-00064691.

XX
 PA (XOMA) XOMA CORP.

XX
 PI Better MD, Carroll SF, Studnicka GM;

XX
 DR WPI; 1995-006804/01.

XX
 PT Polynucleotide(s) encoding type I ribosome-inactivating proteins - which
 PT are suitable for use as components of cytotoxic therapeutic agents.

XX
 PS Example 3; Page 186; 221pp; English.

XX
 CC AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating
 CC protein (RIP) gelonin, one of the nine RIPS described in AAR63903-R63911.
 CC RIPS are key components of cytotoxic therapeutic agents (CTAs), which

CC include gene fusion products and immunoconjugates. CTAs may be used to
 CC selectively eliminate any cell type to which a RIP component is
 CC targeted, by the specific binding capacity of the second component of
 CC the agent. They can be used in the treatment of diseases where the
 CC elimination of a particular cell type is desired, such as autoimmune
 CC disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to
 CC correct PN field.)
 XX
 SQ Sequence 251 AA;

Query Match 99.4%; Score 1279; DB 2; Length 251;
 Best Local Similarity 99.6%; Pred. No. 1.2e-124;
 Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GLDVSFSTKATYITVNFNLRLVKLPENSHGIPLLRKKCDPDKCFVLVALSNDN 60
 DB 1 GLDVSFSTKATYITVNFNLRLVKLPENSHGIPLLRKKCDPDKCFVLVALSNDN 60
 QY 61 GOLABIAIDVTSVYVVGQVRNRSYFFKADPAAYEGLFKNTIKTRLHFGGSPSLEGEK 120
 DB 61 GOLABIAIDVTSVYVVGQVRNRSYFFKADPAAYEGLFKNTIKTRLHFGGSPSLEGEK 120
 QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAARPTFIENQIRNN 180
 DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAARPTFIENQIRNN 180
 QY 181 FOORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
 DB 181 FOORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
 QY 241 ALLKFVDKDPK 251
 DB 241 ALLKFVDKDPK 251

RESULT 11

AAR63918
 ID AAR63918 standard; protein; 251 AA.
 AC AAR63918;
 DT 25-MAR-2003 (revised)
 DT 27-JUL-1995 (first entry)
 XX
 XX Type I RIP gelonin analog Gel (C248).
 DE
 KW Type I ribosome-inactivating proteins; RIPs; gelonin;
 KW cytotoxic therapeutic agents; autoimmune disease; cancer;
 KW graft-versus-host disease.
 XX
 XX Gelonium multiflorum.
 OS
 XX WO9426910-A1.
 PN
 XX 24-NOV-1994.
 PD
 XX 12-MAY-1994; 94WO-US005348.
 PF
 XX 12-MAY-1993; 93US-00064691.
 PR
 XX (XOMA) XOMA CORP.
 PA
 XX Better MD, Carroll SF, Studnicka GM;
 PI
 XX WPI; 1995-006804/01.
 DR
 XX Polynucleotide(s) encoding type I ribosome-inactivating proteins - which
 XX are suitable for use as components of cytotoxic therapeutic agents.
 PT
 XX Example 3; Page 183-184; 221pp; English.
 PS
 XX AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating
 CC protein (RIP) gelonin, one of the nine RIPs described in AAR63903-R63911.

CC RIPs are key components of cytotoxic therapeutic agents (CTAs), which
 CC include gene fusion products and immunoconjugates. CTAs may be used to
 CC selectively eliminate any cell type to which a RIP component is
 CC targeted, by the specific binding capacity of the second component of
 CC the agent. They can be used in the treatment of diseases where the
 CC elimination of a particular cell type is desired, such as autoimmune
 CC disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to
 CC correct PN field.)
 XX
 SQ Sequence 251 AA;

Query Match 99.4%; Score 1279; DB 2; Length 251;
 Best Local Similarity 99.6%; Pred. No. 1.2e-124;
 Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GLDVSFSTKATYITVNFNLRLVKLPENSHGIPLLRKKCDPDKCFVLVALSNDN 60
 DB 1 GLDVSFSTKATYITVNFNLRLVKLPENSHGIPLLRKKCDPDKCFVLVALSNDN 60
 QY 61 GOLABIAIDVTSVYVVGQVRNRSYFFKADPAAYEGLFKNTIKTRLHFGGSPSLEGEK 120
 DB 61 GOLABIAIDVTSVYVVGQVRNRSYFFKADPAAYEGLFKNTIKTRLHFGGSPSLEGEK 120
 QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAARPTFIENQIRNN 180
 DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAARPTFIENQIRNN 180
 QY 181 FOORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
 DB 181 FOORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
 QY 241 ALLKFVDKDPK 251
 DB 241 ALLKFVDKDPK 251

RESULT 12

AAR63920
 ID AAR63920 standard; protein; 251 AA.
 AC AAR63920;
 DT 25-MAR-2003 (revised)
 DT 27-JUL-1995 (first entry)
 XX
 XX Type I RIP gelonin analog Gel (C244).
 DE
 KW Type I ribosome-inactivating proteins; RIPs; gelonin;
 KW cytotoxic therapeutic agents; autoimmune disease; cancer;
 KW graft-versus-host disease.
 XX
 XX Gelonium multiflorum.
 OS
 XX WO9426910-A1.
 PN
 XX 24-NOV-1994.
 PD
 XX 12-MAY-1994; 94WO-US005348.
 PF
 XX 12-MAY-1993; 93US-00064691.
 PR
 XX (XOMA) XOMA CORP.
 PA
 XX Better MD, Carroll SF, Studnicka GM;
 PI
 XX WPI; 1995-006804/01.
 DR
 XX Polynucleotide(s) encoding type I ribosome-inactivating proteins - which
 XX are suitable for use as components of cytotoxic therapeutic agents.
 PT
 XX Example 3; Page 185; 221pp; English.
 PS
 XX AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating
 CC

CC protein (RIP) gelonin, one of the nine RIPs described in AAR63903-R63911.
 CC RIPs are key components of cytotoxic therapeutic agents (CTAs), which
 CC include gene fusion products and immunoconjugates. CTAs may be used to
 CC selectively eliminate any cell type to which a RIP component is
 CC targeted, by the specific binding capacity of the second component of
 CC the agent. They can be used in the treatment of diseases where the
 CC elimination of a particular cell type is desired, such as autoimmune
 CC disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to
 CC correct PN field.)
 XX correct PN field.)
 SQ Sequence 251 AA;

Query Match 99.4%; Score 1279; DB 2; Length 251;
 Best Local Similarity 99.6%; Pred. No. 1.2e-124;
 Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLDTSFSTKGATITTYVNFNLRLVKLPNGNSHGIPLLRKKDDPGKCFVLVALSNDN 60
 |||||
 DB 1 GLDTSFSTKGATITTYVNFNLRLVKLPNGNSHGIPLLRKKDDPGKCFVLVALSNDN 60
 |||||

QY 61 GQLAEIAIDVTSVYVVGQVNRNSYFFKDPADAAVEGLFKNTIKTRLHFGGSYPSLEGK 120
 |||||
 DB 61 GQLAEIAIDVTSVYVVGQVNRNSYFFKDPADAAVEGLFKNTIKTRLHFGGSYPSLEGK 120
 |||||

QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTIEASLLVVIQWSEAAARFTFIENQIRNN 180
 |||||
 DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTIEASLLVVIQWSEAAARFTFIENQIRNN 180
 |||||

QY 181 FOQIRPANNTISLENKWKLSFOIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240
 |||||
 DB 181 FOQIRPANNTISLENKWKLSFOIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240
 |||||

QY 241 ALLKFVDKDPK 251
 |||||
 DB 241 ALLCFVDKDPK 251
 |||||

RESULT 13
 AAR63919
 ID AAR63919 standard; protein; 251 AA.
 XX AAR63919;
 AC AAR63919;
 XX AAR63919;
 DT 25-MAR-2003 (revised)
 DT 27-JUL-1995 (first entry)
 XX Type I RIP gelonin analog Gel (C239).
 XX Type I RIP gelonin analog Gel (C239).
 KW Type I ribosome-inactivating proteins; RIPs; gelonin;
 KW cytotoxic therapeutic agents; autoimmune disease; cancer;
 KW graft-versus-host disease.
 XX Gelonium multiflorum.
 XX Gelonium multiflorum.
 XX WO9426910-A1.
 XX WO9426910-A1.
 PD 24-NOV-1994.
 XX 24-NOV-1994.
 XX 12-MAY-1994; 94WO-US005348.
 XX 12-MAY-1994; 94WO-US005348.
 PR 12-MAY-1993; 93US-00064691.
 XX 12-MAY-1993; 93US-00064691.
 XX (XOMA) XOMA CORP.
 XX (XOMA) XOMA CORP.
 XX Better MD, Carroll SF, Studnicka GM;
 XX Better MD, Carroll SF, Studnicka GM;
 DR WPI; 1995-006804/01.
 XX WPI; 1995-006804/01.
 XX Polynucleotide(s) encoding type I ribosome-inactivating proteins - which
 XX are suitable for use as components of cytotoxic therapeutic agents.
 XX Example 3; Page 184; 221pp; English.
 PS Example 3; Page 184; 221pp; English.

CC AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating
 CC protein (RIP) gelonin, one of the nine RIPs described in AAR63903-R63911.
 CC RIPs are key components of cytotoxic therapeutic agents (CTAs), which
 CC include gene fusion products and immunoconjugates. CTAs may be used to
 CC selectively eliminate any cell type to which a RIP component is
 CC targeted, by the specific binding capacity of the second component of
 CC the agent. They can be used in the treatment of diseases where the
 CC elimination of a particular cell type is desired, such as autoimmune
 CC disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to
 CC correct PN field.)
 XX correct PN field.)
 SQ Sequence 251 AA;

Query Match 99.4%; Score 1279; DB 2; Length 251;
 Best Local Similarity 99.6%; Pred. No. 1.2e-124;
 Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLDTSFSTKGATITTYVNFNLRLVKLPNGNSHGIPLLRKKDDPGKCFVLVALSNDN 60
 |||||
 DB 1 GLDTSFSTKGATITTYVNFNLRLVKLPNGNSHGIPLLRKKDDPGKCFVLVALSNDN 60
 |||||

QY 61 GQLAEIAIDVTSVYVVGQVNRNSYFFKDPADAAVEGLFKNTIKTRLHFGGSYPSLEGK 120
 |||||
 DB 61 GQLAEIAIDVTSVYVVGQVNRNSYFFKDPADAAVEGLFKNTIKTRLHFGGSYPSLEGK 120
 |||||

QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTIEASLLVVIQWSEAAARFTFIENQIRNN 180
 |||||
 DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTIEASLLVVIQWSEAAARFTFIENQIRNN 180
 |||||

QY 181 FOQIRPANNTISLENKWKLSFOIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240
 |||||
 DB 181 FOQIRPANNTISLENKWKLSFOIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240
 |||||

QY 241 ALLKFVDKDPK 251
 |||||
 DB 241 ALLKFVDKDPK 251
 |||||

RESULT 14
 AAR63924
 ID AAR63924 standard; protein; 251 AA.
 XX AAR63924;
 AC AAR63924;
 XX AAR63924;
 DT 25-MAR-2003 (revised)
 DT 27-JUL-1995 (first entry)
 XX Type I RIP gelonin analog Gel (C184).
 XX Type I RIP gelonin analog Gel (C184).
 KW Type I ribosome-inactivating proteins; RIPs; gelonin;
 KW cytotoxic therapeutic agents; autoimmune disease; cancer;
 KW graft-versus-host disease.
 XX Gelonium multiflorum.
 XX Gelonium multiflorum.
 XX WO9426910-A1.
 XX WO9426910-A1.
 PD 24-NOV-1994.
 XX 24-NOV-1994.
 XX 12-MAY-1994; 94WO-US005348.
 XX 12-MAY-1994; 94WO-US005348.
 PR 12-MAY-1993; 93US-00064691.
 XX 12-MAY-1993; 93US-00064691.
 XX (XOMA) XOMA CORP.
 XX (XOMA) XOMA CORP.
 XX Better MD, Carroll SF, Studnicka GM;
 XX Better MD, Carroll SF, Studnicka GM;
 DR WPI; 1995-006804/01.
 XX WPI; 1995-006804/01.
 XX Polynucleotide(s) encoding type I ribosome-inactivating proteins - which
 XX are suitable for use as components of cytotoxic therapeutic agents.
 XX Example 3; Page 188-189; 221pp; English.
 PS Example 3; Page 188-189; 221pp; English.

XX AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating
 CC protein (RIP) gelonin, one of the nine RIPs described in AAR63903-R63911.
 CC RIPs are key components of cytotoxic therapeutic agents (CTAs), which
 CC include gene fusion products and immunoconjugates. CTAs may be used to
 CC selectively eliminate any cell type to which a RIP component is
 CC targeted, by the specific binding capacity of the second component of
 CC the agent. They can be used in the treatment of diseases where the
 CC elimination of a particular cell type is desired, such as autoimmune
 CC disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to
 CC correct PN field.)
 XX Sequence 251 AA;
 SQ

Query Match 99.4%; Score 1279; DB 2; Length 251;
 Best Local Similarity 99.6%; Pred. No. 1.2e-124; Indels 0; Gaps 0;
 Matches 250; Conservative 0; Mismatches 1;

QY 1 GLDTSVSTKGATITTYVNFNLRLVKLPKPGNSHGIPLLRKKDDPGKCFVLVALSNDN 60
 DB 1 GLDTSVSTKGATITTYVNFNLRLVKLPKPGNSHGIPLLRKKDDPGKCFVLVALSNDN 60
 QY 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKADPAAYEGLFKNTIKTRLHFGGSSPSLEGEK 120
 DB 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKADPAAYEGLFKNTIKTRLHFGGSSPSLEGEK 120
 QY 121 AYRETTDLGIEPLRIGIKKLDENAIQNYKPTIASLLVVIQMVSEAAARFTFIENQIRNN 180
 DB 121 AYRETTDLGIEPLRIGIKKLDENAIQNYKPTIASLLVVIQMVSEAAARFTFIENQIRNN 180
 QY 181 FQOIRPANNTISLENKWGKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
 DB 181 FQOIRPANNTISLENKWGKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
 QY 241 ALLKFVDKDPK 251
 DB 241 ALLKFVDKDPK 251

RESULT 15

AAR63922
 ID AAR63922 standard; protein; 251 AA.

XX AC AAR63922;

XX 25-MAR-2003 (revised)

XX 27-JUL-1995 (first entry)

XX DE Type I RIP gelonin analog Gel(c60).

XX KW Type I ribosome-inactivating proteins; RIPs; gelonin;
 KW cytotoxic therapeutic agents; autoimmune disease; cancer;
 KW graft-versus-host disease.

XX OS Gelonium multiflorum.

XX PN WO9426910-A1.

XX PD 24-NOV-1994.

XX PF 12-MAY-1994; 94WO-US005348.

XX PR 12-MAY-1993; 93US-00064691.

XX PA (XOMA) XOMA CORP.

XX PI Better MD, Carroll SF, Studnicka GM;

XX DR WPI; 1995-006804/01.

XX PT Polynucleotide(s) encoding type I ribosome-inactivating proteins - which
 XX are suitable for use as components of cytotoxic therapeutic agents.

PS Example 3; Page 187; 221pp; English.

XX AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating
 CC protein (RIP) gelonin, one of the nine RIPs described in AAR63903-R63911.
 CC RIPs are key components of cytotoxic therapeutic agents (CTAs), which
 CC include gene fusion products and immunoconjugates. CTAs may be used to
 CC selectively eliminate any cell type to which a RIP component is
 CC targeted, by the specific binding capacity of the second component of
 CC the agent. They can be used in the treatment of diseases where the
 CC elimination of a particular cell type is desired, such as autoimmune
 CC disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to
 CC correct PN field.)
 XX Sequence 251 AA;
 SQ

Query Match 99.3%; Score 1278; DB 2; Length 251;
 Best Local Similarity 99.6%; Pred. No. 1.6e-124; Indels 0; Gaps 0;
 Matches 250; Conservative 0; Mismatches 1;

QY 1 GLDTSVSTKGATITTYVNFNLRLVKLPKPGNSHGIPLLRKKDDPGKCFVLVALSNDN 60
 DB 1 GLDTSVSTKGATITTYVNFNLRLVKLPKPGNSHGIPLLRKKDDPGKCFVLVALSNDN 60
 QY 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKADPAAYEGLFKNTIKTRLHFGGSSPSLEGEK 120
 DB 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKADPAAYEGLFKNTIKTRLHFGGSSPSLEGEK 120
 QY 121 AYRETTDLGIEPLRIGIKKLDENAIQNYKPTIASLLVVIQMVSEAAARFTFIENQIRNN 180
 DB 121 AYRETTDLGIEPLRIGIKKLDENAIQNYKPTIASLLVVIQMVSEAAARFTFIENQIRNN 180
 QY 181 FQOIRPANNTISLENKWGKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
 DB 181 FQOIRPANNTISLENKWGKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
 QY 241 ALLKFVDKDPK 251
 DB 241 ALLKFVDKDPK 251

Search completed: February 10, 2006, 10:04:59

Job time : 138.614 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 10, 2006, 10:05:19 ; Search time 34.2694 Seconds
(without alignments)
704.723 Million cell updates/sec

Title: US-10-717-243-2

Perfect score: 1287

Sequence: 1 GLDTSVSTKGTATYTYNPF.....AVDQVKPKALKKFVDKDPK 251

Scoring table:

BL0SUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 80: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1287	100.0	316	2	JT0753
2	348.5	27.1	245	2	JC4840
3	346	26.9	286	2	S25560
4	343	26.7	576	1	RLCSD
5	341	26.5	286	2	JC4235
6	334.5	26.0	564	1	RLCSAG
7	333.5	25.9	527	2	S32430
8	330.5	25.7	294	2	S28421
9	329	25.6	251	2	C39761
10	325	25.3	313	2	SI7757
11	321	24.9	289	1	RLPZT
12	320	24.9	528	1	TZLSA
13	315	24.5	247	2	JU0393
14	315	24.5	289	2	JCS606
15	311.5	24.2	261	2	JE0401
16	310	24.1	247	2	JCS032
17	306.5	23.8	277	2	S22494
18	300.5	23.3	254	2	PD0018
19	298	23.2	528	2	S32431
20	298	23.2	562	2	SI6022
21	291	22.6	286	1	RLPUGG
22	287.5	22.3	570	2	S62627
23	283.5	22.0	278	2	S23519
24	270	21.0	250	2	JN0108
25	215.5	16.7	278	2	A39817
26	210	16.3	272	2	JC4811
27	202	15.7	310	2	S46239
28	195	15.2	40	2	SI7574
29	181.5	14.1	253	2	S28542

30 181.5 14.1 292 1 RLQHG2 rRNA N-glycosidase
31 181 14.1 289 2 TI2573 rRNA N-glycosidase
32 179 13.9 293 2 SI7519 rRNA N-glycosidase
33 177.5 13.8 283 2 S05205 rRNA N-glycosidase
34 176.5 13.7 253 2 S28541 rRNA N-glycosidase
35 176.5 13.7 253 2 S28539 rRNA N-glycosidase
36 176.5 13.7 253 2 S29931 rRNA N-glycosidase
37 171.5 13.3 253 2 AS8923 rRNA N-glycosidase
38 149 11.6 236 2 SI7932 rRNA N-glycosidase
39 121 9.4 106 2 B39761 abrin (clone 3.7)
40 120.5 9.4 1948 2 B69511 N conserved hypoch
41 114.5 8.9 275 2 S33631 tritin - wheat
42 113.5 8.8 280 1 RL6H rRNA N-glycosidase
43 104.5 8.1 281 2 B38664 30K ribosome inact
44 103 8.0 280 2 JC5848 protein synthesis
45 102.5 8.0 456 2 T05612 hypothetical prote

ALIGNMENTS

RESULT 1

JT0753

rRNA N-glycosidase (EC 3.2.2.22) precursor - Gelonium multiflorum

N:Alternate names: gelonin; type I ribosome-inactivating protein

C:Species: Gelonium multiflorum

C>Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 09-Jul-2004

C:Accession: JT0753; SI6489

R:Nolan, P.A.; Garrison, D.A.; Better, M.

Gene 134, 223-227, 1993

A:Title: Cloning and expression of a gene encoding gelonin, a ribosome-inactivating prot

A:Reference number: JT0753; MUID:94085781; PMID:7916721

A:Accession: JT0753

A:Molecule type: mRNA

A:Residues: 1-316 <NOL>

A:Cross-references: UNIPROT:P3186; UNIPARC:UPI0000133948; GB:L12243; NID:9388633; PDB:1

R:Montecucchi, P.C.; Lazzarini, A.M.; Barbieri, L.; Stripe, P.; Sorla, M.; Lappi, D.

Int. J. Pept. Protein Res. 33, 263-267, 1989

A:Title: N-terminal sequence of some ribosome-inactivating proteins.

A:Reference number: SI6331; MUID:89326691; PMID:2753596

A:Accession: SI6489

A:Molecule type: protein

A:Residues: 47-89, 'K', '91-92, 'D' <MON>

A:Cross-references: UNIPARC:UPI0000177F26

C:Function:

A:Description: hydrolyzes the N-glycosidic bond of a specific adenosine in 28S rRNA the

C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology

C:Keywords: glycosidase; hydrolase

F:1-46/Domain: signal sequence #status predicted <SIG>

F:47-316/Product: ribosomal RNA N-glycosidase #status predicted <MAT>

F:53-294/Domain: rRNA N-glycosidase homology <RNG>

Query Match 100.0%; Score 1287; DB 2; Length 316;

Best Local Similarity 100.0%; Pred. No. 1.3e-100;

Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLDTSVSTKGTATYTYNPFNLRLVKLPKGNHGIPLLRKCKDDPKCFVLVALSNDN 60

Db 47 GLDTSVSTKGTATYTYNPFNLRLVKLPKGNHGIPLLRKCKDDPKCFVLVALSNDN 106

QY 61 GOLAEIAIDVTSVYVGVQVNRNSYFPKADPAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120

Db 107 GOLAEIAIDVTSVYVGVQVNRNSYFPKADPAAYEGLFKNTIKTRLHFGGSYPSLEGEK 166

QY 121 AYRTTDLGIBPLRIGIKLKDENAIDNPKPTIASSLLVWIQMSEARPTFIENQIRNN 180

Db 167 AYRTTDLGIBPLRIGIKLKDENAIDNPKPTIASSLLVWIQMSEARPTFIENQIRNN 226

QY 181 FQQRIRPANNTISLENKWKLSFOIRTSNGMFMSEAVELERANGKYYVTAVDQVKPKI 240

Db 227 FQQRIRPANNTISLENKWKLSFOIRTSNGMFMSEAVELERANGKYYVTAVDQVKPKI 286

QY 241 ALLKFFVDKDPK 251

J. Biol. Chem. 260, 15682-15686, 1985
A>Title: The primary sequence of Ricinus communis agglutinin. Comparison with ricin.
A:Reference number: A24261; MUID:86059449; PMID:2999130
A:Accession: A24261
A:Molecule type: mRNA
A:Residues: 1-564 <ROR>
A:CROSS-references: UNIPROT:P06750; UNIPARC:UPI0000125689; GB:M12089; NID:g169700; PIDN:
R:Araki, T.; Yoshitaka, Y.; Funatsu, G.
Biochim. Biophys. Acta 872, 277-285, 1986
A>Title: The complete amino acid sequence of the B-chain of the Ricinus communis aggluti
A:Reference number: A24210
A:Accession: A24210
A:Molecule type: protein
A:Residues: 303-325, 'F', 327-330, 'T', 332-361, 'D', 363-373, 'G', 375-403, 'T', 405-551, 'V', 553-
A:CROSS-references: UNIPARC:UPI0000174679
A:Comment: This protein has strong agglutinating activity and weak cytotoxicity compared
C:Superfamily: ricin; rRNA N-glycosidase homology
C:Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; RNA binding; seed
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-290/Product: agglutinin chain A #status predicted <ACH>
F:35-281/Domain: rRNA N-glycosidase homology <RNG>
F:303-564/Product: agglutinin chain B #status experimental <BCH>
F:319-361,362-402,405-443,450-485,489-528,531-564/Region: 40-residue repeats
F:34,259/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:104,147,231,232/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F:200,203/Active site: Glu, Arg #status predicted
F:282-306,322-341,365-382,453-466,492-509/Disulfide bonds: #status predicted
F:324,337,348/Binding site: N-acetylgalactosamine (Asp, Glu, Asn) #status predicted
F:397,437/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:536,557/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted

Query Match 26.0%; Score 334.5; DB 1; Length 564;
Best Local Similarity 36.3%; Pred. No. 3.2e-20;
Matches 91; Conservative 42; Mismatches 105; Indels 13; Gaps 7;

QY 5 VPSFTKGATYYTYNFMELRVKLPKGN-SHGIPLLKKCCDDP-GKCFVLVALSNDNGQ 62
DB 33 INFTTADATVSYTYTFIRAVRSHLTGTGADVRHIEVPLNRVGLFISQRFILVELSNHAE 92
QY 63 LAEIAIDVTSVVGVGYVRNRSYFFKADP-----AAVEGLFKNTIKT-RLHFSGSYPSL 116
DB 93 SVTLALDVTNAVVCGRAGNSAYFFH--PDNQEDAEATHLFTDVQNSFTFAFGGNYDEL 150
QY 117 EGKEYARETTDLGIEPLRIGIKKLDENADINYKPTETIASLLVVIQMVSEAAARFTPINQ 176
DB 151 EQLGGLRENIELGTGLEDAISALYYSTCGTQIPTLARSFWVCIMISEAARFOYIEGE 210
QY 177 IRN--NFQORIRPANNTISLENKWKLSFQIRTSANGAMFSEAVELERANGKYYVTAVD 234
DB 211 MKRIRYNNRSAPDPSVITLNSWGRLSTAQESN-QGAFASPIQLQRRNGSKFNVDVS 269
QY 235 QVKPKIALKLF 245
DB 270 ILIPIALVMY 280

RESULT 7
S32430
abrin-b precursor - Indian licorice (fragment)
N:Contains: rRNA N-glycosidase (EC 3.2.2.22)
C:Species: Abrus precatorius (Indian licorice)
C>Date: 30-Sep-1993 #sequence_revision 01-Aug-1997 #text_change 09-Jul-2004
C:Accession: S32430; JCI1399
R:Hung, C.H.; Lee, M.C.; Lee, T.C.; Lin, J.Y.
J. Mol. Biol. 229, 263-267, 1993
A>Title: Primary structure of three distinct isoabirins determined by cDNA sequencing. Co
A:Reference number: S32429; MUID:93132798; PMID:8421313
A:Accession: S32430
A:Molecule type: mRNA
A:Residues: 1-527 <HUN>
A:CROSS-references: UNIPROT:Q06077; UNIPARC:UPI0000125160; GB:M98345; NID:g166296; PIDN:
R:Kimura, M.; Sumizawa, T.; Funatsu, G.
Biochem. Biotechnol. Biochem. 57, 166-169, 1993

A>Title: The complete amino acid sequences of the B-chains of Abrin-a and Abrin-b, toxic
A:Reference number: JCI1398; MUID:93169023; PMID:7763422
A:Accession: JCI1399
A:Molecule type: protein
A:Residues: 260-281, 'D', 283-290, 'N', 292-349, 'PQ', 352-377, 'N', 379-425, 'M', 427, 'D', 429-430
A:CROSS-references: UNIPARC:UPI0000177F2A
A:Experimental source: seed
C:Superfamily: ricin; rRNA N-glycosidase homology
C:Keywords: disulfide bond; duplication; glycoprotein; glycosidase; hydrolase; lectin; p
F:1-250/Product: abrin-b chain A #status predicted <ACH>
F:7-245/Domain: rRNA N-glycosidase homology <RNG>
F:260-527/Product: abrin-b chain B #status experimental <BCH>
F:282-324,325-365,368-406,413-448,452-491,494-527/Region: 40-residue repeats
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
F:174,113,194,195/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F:110,360,400/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:163,166/Active site: Glu, Arg #status predicted
F:246-268,285-304,328-345,416-429,455-472/Disulfide bonds: #status predicted
F:287,311/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted
F:499,520/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted

Query Match 25.9%; Score 333.5; DB 2; Length 527;
Best Local Similarity 37.7%; Pred. No. 3.5e-20;
Matches 97; Conservative 34; Mismatches 103; Indels 23; Gaps 9;

QY 5 VPSFTKGATYYTYNFMELRVKLPKGN-SHGIPLLKKCCDDPDKC-----FVLVALSND 59
DB 5 IKFTTEGATSQYKQFTEALRQL-TGGLIHGIPVL-----PDPTTLOERNYIISVELSNS 59
QY 60 NGQLAETAITDVTSVVGVGYVRNRSYFFKADPDAAYEGLPKNTIKTRLHFSGSYPSLEG- 118
DB 60 DTESIEAGIDVSNAYVAYRAGNRSYFLRDAPTSASRYLFTGTQOYSLRFGNSYIDLRL 119
QY 119 EKAYRETTDLGIEPLRIGIKKLDENADINYKPTETIASLLVVIQMVSEAAARFTPIENO-- 176
DB 120 ARQTRQOPIPLGLQALRHAIPLQSGTDQ-----EIARTLIVIIQWSEAAARFYISYRVG 175
QY 177 --IRNFFQORIRPANNTISLENKWKLSFQIRTSANGAMFSEAVELERANGKYYVTAV- 233
DB 176 VSIRTN--TAFQPDAAIMISLENNWDLNLSGGVQQS-VODTFPNAVTLRSVNNQPVIVDSL 232
QY 234 DQVKPKIALKFKVDKP 250
DB 233 HQSVAVLALMFLVCNPP 249

RESULT 8
S28421
rRNA N-glycosidase (EC 3.2.2.22) PAP-alpha - Virginian pokeweed
N:Alternate names: antiviral protein alpha-PAP
C:Species: Phytolacca americana (Virginian pokeweed)
C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C:Accession: S28421
R:Kataoka, J.; Habuka, N.; Masuta, C.; Miyano, M.; Koiwai, A.
Plant Mol. Biol. 20, 879-886, 1992
A>Title: Isolation and analysis of a genomic clone encoding a pokeweed antiviral protein
A:Reference number: S28421; MUID:93099240; PMID:1281438
A:Accession: S28421
A:Molecule type: DNA
A:Residues: 1-294 <KAT>
A:CROSS-references: UNIPROT:Q03464; UNIPARC:UPI0000133946; EMBL:D10600; NID:g218010; PID
C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
C:Keywords: Glycosidase; hydrolase
F:30-278/Domain: rRNA N-glycosidase homology <RNG>

Query Match 25.7%; Score 330.5; DB 2; Length 294;
Best Local Similarity 32.2%; Pred. No. 2.9e-20;
Matches 85; Conservative 50; Mismatches 102; Indels 27; Gaps 8;

QY 2 LDTVSTFKGATYYTYNFMELRVKLPKGN-SHGIPLLKKCCDDPDKCFVLVALSNDN 60
DB 25 INTITFDVGNATINKYATFMKSIHQAQDPTLKCVCYIPMLPNTLTPK--YLLVTLQDSS 82

QY 61 GQLABIAIDVTSVYVVG-----YQVNRSYFFKDAADAAVEGLFKVTKITRL----- 107
Db 83 LKTIITMLKRNLYVMGYADTYNGKRVHPKDISNTTE-----RNDVMTILCPNPSRVG 138
QY 108 ---HFGGSPSLEGKAY-RETTDLGIEPLRIGIKKLDENADNYKPTIASSLLWVQM 163
Db 139 KNINDSSYPALKKKVGRPSQVQIGIQLNSGIGKI--YGVDSFTKTEAEFLVALQM 196
QY 164 VSEAAARFTFIENQIRNFQORIRPANNTISLENKWKLSFQIRTSKGANGMSEAVEVLR 223
Db 197 VSEAAARFKYIENQVNTFNRAFPNAPKVLNLEESWGLKSTAIH-NAKNGALTSPLKNA 255
QY 224 NGKKYVYVAVDQVKPAILLKVD 247
Db 256 NGSKWILVRVDDIEBPDVGLLKYN 279
RESULT 9
C39761
abrin (clone 7.2) precursor - Indian licorice (fragment)
N:Contains: rRNA N-glycosidase (EC 3.2.2.22)
C:Species: Abrus precatorius (Indian licorice)
C:Date: 21-Feb-1992 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C:Accession: C39761; S14471
R:Evensen, G.; Mathiesen, A.; Sundan, A.
J. Biol. Chem. 266, 6848-6852, 1991
A:Title: Direct molecular cloning and expression of two distinct abrin A-chains.
A:Reference number: A39761; MUID:91201329; PMID:2016300
A:Accession: C39761
A:Molecule type: DNA
A:Residues: 1-251 <EV>
A:Cross-references: UNIPROT:Q38760; UNIPARC:UPI0000177F2F
R:Evensen, G.; Mathiesen, A.; Sundan, A.
submitted to the EMBL Data Library, October 1990
A:Description: Direct molecular cloning of two distinct abrin A-chains.
A:Reference number: S14471
A:Accession: S14471
A:Molecule type: DNA
A:Residues: 'M', 1-251 <EV>
A:Cross-references: UNIPARC:UPI0000AAB08; EMBL:X54872; NID:g16088; PIDN:CAA38654.1; PID
C:Superfamily: ricin; rRNA N-glycosidase homology
C:Keywords: duplication; glycosidase; hydrolase; lectin; toxin
F:1-251/Product: abrin (clone 7.2) chain A #status predicted <ACH>
F:7-246/Domain: rRNA N-glycosidase homology <RNG>
F:74,113,195,196/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F:164,167/Active site: Glu, Arg #status predicted
Query Match 25.6%; Score 329; DB 2; Length 251;
Best Local Similarity 36.5%; Pred. No. 3.1e-20;
Matches 93; Conservative 40; Mismatches 104; Indels 18; Gaps 8;
QY 5 VSFSTKGATYITYVNFNLRLVKLPKPGNSHGIPLLRKKCDPDGKC-----PVLVALSND 59
Db 5 IKFSTEGATOSYKQFIALRERLR-GLLIHDIPVLR-----DPTVBERNYITVELSNS 59
QY 60 NGQLABIAIDVTSVYVVGQVNRSYFFKDAADAAVEGLFKNTIKTRLHFGGSPSLR-G 118
Db 60 ERESIEVGIDVTNAVVAIRAGSQSYFLRDAPASASTVLTCTQYSLRFDGSGYDLERW 119
QY 119 EKAYRETTDLGIEPLRIGIKKLDENADNYKPTIASSLLWVQMSEAAARFTFIENQIR 178
Db 120 AHQTEQISLGLQALTHAISPLRSASND---EEKARTLIVLIQWASAAARVRYISNRVG 176
QY 179 NNQF--QIRPANNTISLENKWKLSFQIRTSKGANGMSEAVEVLRANKKYVYVAV-DQ 235
Db 177 VSRITGTAFPQDPAMLSLENNWINDISRGVQBS-VQDTFPNAVTLRVRNNQPVIVDSLTHQ 235
QY 236 VKPIALKLFVDKOP 250
Db 236 SVALALMLFVCNPP 250
RESULT 10

S17757
rRNA N-glycosidase (EC 3.2.2.22) PAP precursor - Virginian pokeweed
N:Alternate names: pokeweed antiviral protein; protein synthesis inhibitor; ribosome-in-
C:Species: Phytolacca americana (Virginian pokeweed)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C:Accession: S17757; S02792; S13469; S32611
R:Lin, Q.; Chen, Z.C.; Antoniw, J.F.; White, R.F.
Plant Mol. Biol. 17, 609-614, 1991
A:Title: Isolation and characterization of a cDNA clone encoding the anti-viral protein
A:Reference number: S17757; MUID:92003676; PMID:1912488
A:Accession: S17757
A:Molecule type: DNA
A:Residues: 1-313 <LIN>
A:Cross-references: UNIPROT:P10297; UNIPARC:UPI0000133932; EMBL:X55383; NID:g20421; PIDN
R:Barbieri, L.; Bolognesi, A.; Cenini, P.; Falasca, A.I.; Minghetti, A.; Garofano, L.; C
Biochem. J. 257, 801-807, 1989
A:Title: Ribosome-inactivating proteins from plant cells in culture.
A:Reference number: S02792; MUID:89193489; PMID:2930487
A:Accession: S02792
A:Molecule type: Protein
A:Residues: 23-55, 'X', 57-65 <BAR>
A:Cross-references: UNIPARC:UPI0000177F24
R:Bolognesi, A.; Barbieri, L.; Abbondanza, A.; Falasca, A.I.; Carnicelli, D.; Battelli,
Biochim. Biophys. Acta 1087, 293-302, 1990
A:Title: Purification and properties of new ribosome-inactivating proteins with RNA N-g
A:Reference number: S13469; MUID:91064383; PMID:2248976
A:Accession: S13469
A:Molecule type: Protein
A:Residues: 23-54 <BO>
A:Cross-references: UNIPARC:UPI0000177F25
R:BJorn, M.J.; Larrick, J.; Piatak, M.; Wilson, K.J.
Biochim. Biophys. Acta 790, 154-163, 1984
A:Title: Characterization of translational inhibitors from Phytolacca americana. Amino-t
A:Reference number: S32610; MUID:85023392; PMID:6091760
A:Accession: S32611
A:Molecule type: Protein
A:Residues: 23-54 <BJO>
A:Cross-references: UNIPARC:UPI0000177F25
C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
C:Keywords: glycosidase; hydrolase
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-313/Product: rRNA N-glycosidase PAP #status experimental <MAT>
F:128-277/Domain: rRNA N-glycosidase homology <RNG>
Query Match 25.3%; Score 325; DB 2; Length 313;
Best Local Similarity 31.6%; Pred. No. 9.1e-20;
Matches 84; Conservative 49; Mismatches 101; Indels 32; Gaps 8;
QY 2 LDTVSFSTKGATYITYVNFNLRLVKLK-PGNSHGIPLLRKKDDPKCFVLVALSNDN 60
Db 23 VNTIIVNGVSTTISKYATFLNLRNEAKDPSLKCVGIPMLPNTNPK--YVVELQGSN 80
QY 61 GQLABIAIDVTSVYVVGQ-----VNRSYFFK-----APDAAYEGLFKNT 102
Db 81 KKTITLMLRNLNLYVMGYSDPFTNCKRYHIFNDISGTERQDVETTLCPNA-----NSR 134
QY 103 IKTRLHFGGSPSLEGKAY--RETTDLGIEPLRIGIKKLDENADNYKPTIASSLLAV 160
Db 135 VSKNINDFSRPTUESKAGVKSQVQIGIQLNSNGKI--SGVMSSTKTEAEFLVA 192
QY 161 IQMVSEAAARFTFIENQIRNFQORIRPANNTISLENKWKLSFQIRTSKGANGMSEAVEV 220
Db 193 IQMVSEAAARFKYIENQVNTFNRAFPNAPKVLNLEQETWGLKSTAIH-DAKNGVLPKPLEL 251
QY 221 ERANGKKYVYVAVDQVKPAILLKPV 246
Db 252 VDASGAKWILVRVDEIKPDVALLNV 277
RESULT 11
RLT2T
rRNA N-glycosidase (EC 3.2.2.22) alpha-trichosanthin precursor [validated] - Mongolian s
N:Alternate names: alpha-TCS; type I ribosome-inactivating protein

F;93,183,186/Active site: Tyr, Glu, Arg #status predicted

Query Match 24.9%; Score 321.; DB 1; Length 289;
Best Local Similarity 37.8%; Pred. No. 1.8e-19;
Matches 93; Conservative 35; Mismatches 104; Indels 14; Gaps 8;

QY 5 VFSSTKGATYYTVVFNELRVKLKPEGNSHGIPILLRKKCDPFG-KCFVLVALSNDNGQL 63
||| ||| : : : || : : : || : : : || : : : || : : : || : : :
Db 25 VSPRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSL--PGSQRYALIHLTNTVADET 82
||| ||| : : : || : : : || : : : || : : : || : : : || : : :
QY 64 AETAIDVTSVVVGYQVRNRSYFFKDA-PDAAYEGLFKNYI-KTRLHFHGSYSYLE-GEK 120
||| ||| : : : || : : : || : : : || : : : || : : : || : : :
Db 83 ISVAIDVTNVINGYRAGTSTPYFNEASATEAAKYVFDMARKVTLPYSGNYERLOTAAG 142
||| ||| : : : || : : : || : : : || : : : || : : : || : : :
QY 121 AVRETTDLGTPLRIGIKKLDENAIDNYKPTETASSLLVVIVQMVEAARFTFIENQIRNN 180
||| ||| : : : || : : : || : : : || : : : || : : : || : : :
Db 143 KIRENPGLGPLDSAI-----TTLFYVNANSASALMWLIQTSEARYKFIEQQIGKR 197
||| ||| : : : || : : : || : : : || : : : || : : : || : : :
QY 181 FQOIRPANNTISLENKWKLSQPISR-TSGANGMFSEAVELEERANGKKYVYTAVDQ--VK 237
||| ||| : : : || : : : || : : : || : : : || : : : || : : :
Db 198 VDKTFPLSLAISLENSWALSQKIQAISTNNGQSFESPVVLINAQNRVTITNVDAVGWVT 257
||| ||| : : : || : : : || : : : || : : : || : : : || : : :
QY 238 PKIALL 243
||||
Db 258 SNIALL 263
||||

RESULT 12

TZLSA
abrin-a precursor - Indian licorice (fragment)
N;Contains: rRNA N-glycosidase (EC 3.2.2.22)
C;Species: Abrus precatorius (Indian licorice)
C;Date: 31-Dec-1993 #sequence revision 01-Aug-1997 #text change 09-Jul-2004
C;Accession: S32429; J70202; A39761; JC1398; S14472; S24133; S74110; S74111
R;Hung, C.H.; Lee, M.C.; Lee, T.C.; Lin, J.Y.
J. Mol. Biol. 229, 263-267, 1993
A;Title: Primary structure of three distinct isoabrins determined by cDNA sequencing
A;Reference number: S32429; MUID:93132798; PMID:8421313
A;Accession: S32429
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 'E',2-528 <HUN>
A;Cross-references: UNIPROT:P11140; UNIPARC:UIPI00001GDA00; GB:M98344; NID:g1662
A;Note: the coding region for the sequence shown is preceded by an ATG codon
A;Note: residues 1-8 were derived from the synthesized primer
R;Funatsu, G.; Taguchi, Y.; Kamenosono, M.; Yanaka, M.
Agric. Biol. Chem. 52, 1095-1097, 1988
A;Title: The complete amino acid sequence of the A-chain of abrin-a, a toxic protein
A;Reference number: J70202
A;Accession: J70202
A;Molecule type: protein
A;Residues: 1-201,203-251 <FUN>
A;Cross-references: UNIPARC:UIPI000017467A
A;Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore R;Byenssen, G.; Mathiesen, A.; Sundan, A.
J. Rvsnsl. Chem. 266, 6848-6852, 1991
A;Title: Direct molecular cloning and expression of two distinct abrin A-chains
A;Reference number: A39761; MUID:91201329; PMID:2016300
A;Accession: A39761
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 'E',2-251 <EVS>
A;Cross-references: UNIPARC:UIPI000011046A; GB:X54872
A;Note: residues 1-8 were derived from the synthesized primer
R;Kimura, M.; Sumizawa, T.; Funatsu, G.
Biosci. Biotechnol. Biochen. 57, 166-169, 1993
A;Title: The complete amino acid sequences of the B-chains of Abrin-a and Abrin-b
A;Reference number: JC1398; MUID:93169023; PMID:7763422
A;Contents: seeds
A;Accession: JC1398
A;Molecule type: protein
A;Residues: 261-347, 'T',349-351,'A',353-357,'L',359-528 <KIM>
A;Cross-references: UNIPARC:UIPI000017467B

A;Experimental source: seed
R;Evensen, G.; Mathiesen, A.; Sundan, A.
submitted to the EMBL Data Library, October 1990
A;Description: Direct molecular cloning of two distinct abrin A-chains.
A;Reference number: S14471
A;Accession: S14472
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 'ME', 2-251 <EV2>
A;Cross-references: UNIPARC:UPI00000ACAB6; EMBL:X54873; NID:g16090; PIDN:CAA38655.1; PII:
R;Chen, Y.L.; Chow, L.P.; Taugita, A.; Lin, J.Y.
FEBS Lett. 309, 115-118, 1992
A;Title: The complete primary structure of abrin-a B chain.
A;Reference number: S24133; MUID:92371656; PMID:1505674
A;Accession: S24133
A;Molecule type: protein
A;Residues: 262-297, 'Y', 299-426, 'L', 428-466, 'P', 468-482, 'L', 484-528 <CH>
A;Cross-references: UNIPARC:UPI000017467C
R;Lin, S.H.; Chow, L.P.; Chen, Y.L.; Liaw, Y.C.; Chen, J.K.; Lin, J.Y.
Eur. J. Biochem. 240, 564-569, 1996
A;Title: Probing the domain structure of abrin-a by tryptic digestion.
A;Reference number: S74110; MUID:97008945; PMID:8856055
A;Accession: S74110
A;Molecule type: protein
A;Residues: 262-276, 'X', 278-280, 329-348, 369-388, 399-418
A;Cross-references: UNIPARC:UPI000017467F; UNIPARC:UPI0000174680; UNIPARC:UPI0000174681
A;Experimental source: seed
C;Comment: Abrin-a is more toxic than ricin. The toxin consists of an A chain, which inh
taining receptors on the cell surface. The A and B chains are linked by a single disulf
C;Superfamily: ricin; rRNA N-glycosidase homology
C;Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; pyroglutamic acid
P;1-251/Product: abrin-a chain A #status experimental <CH>
P;7-246/Domain: rRNA N-glycosidase homology <RG>
P;261-528/Product: abrin-a chain B #status experimental <BC>
P;283-325, 326-366, 369-407, 414-449, 453-492, 495-528/Region: 40-residue repeats
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;74,113,195,196/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F;164,167/Active site: Glu, Arg #status predicted
P;247-269, 286-305, 329-346, 417-430, 456-473/Disulfide bonds: #status predicted
P;288,312/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted
F;361,401/Binding site: carbonylated (Asn) (covalent) #status experimental
F;500,521/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted

Query Match 24.9% Score 320; DB 1; Length 528;
Best Local Similarity 35.7%; Pred. No. 4.8e-19;
Matches 91; Conservative 39; Mismatches 107; Indels 18; Gaps 8;

Qy 5 VSFSTKGATITYVNFALNELRVLKPENSGHGIPLRLKCKDPCGK-----FVLVALSND 59
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 5 IKFSTEGATGSQYKQFTALRERLR--GGLIHDIPVL----PDPTTLQERNRYITVELSNS 59
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 60 NGQLAEIADIVTSVYVGVQVRNSYFFKADPAADAEGLFKNTIKTLHPFGGSYPSLE-G 118
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 60 DTESIIEGIDVTWYVAYVYAGTQSYFLRDPSSADYLFDTGDQHSPLPYGYGLERW 119
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 119 EKAYRETTDLGIEPLRIGIKKLDENAIDNPKPTFIASSLLAVIQWYSEAAARFFIENR 178
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 120 AHQSRQIPLGLQALTHGISFFPSGGNDN--BEKARTLVIIQWAEARFYIENRR 176
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 179 NNQF--ORIRPANNTISLENKWKLSFQIRTSYGANGFSEAVLERANGKYYVTVAQD- 235
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 177 VSIQTGTAFQPDAAWISLENNWNLNRGVQSS-VQDTFFPNQVTLTIRNEPVIIVDSLSHP 235
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 236 VKPKIALLKVFVDKDP 250
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 236 TVAVLALMLFVCNPP 250
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 13

JU0393
karasurin - Mongolian snake-gourd
C;Species: Trichosanthes kirilowii (Mongolian snake-gourd)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: JU0393; PS0163
R;Toyokawa, S.; Takeda, T.; Kato, Y.; Wakabayashi, K.; Ogiwara, Y.
Chen. Pharm. Bull. 39, 1244-1249, 1991
A;Title: The complete amino acid sequence of an abortifacient protein, karasurin.
A;Reference number: JU0393; MUID:92005921; PMID:1914000
A;Accession: JU0393
A;Molecule type: protein
A;Residues: 1-247 <TOY>
A;Cross-references: UNIPROT:P24478; UNIPARC:UPI000015667C
A;Note: A sequence which lacks Ala-247 is also shown in this publication
C;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
C;Keywords: abortifacient
F;4-243/Domain: rRNA N-glycosidase homology <RNG>

Query Match 24.5%; Score 315; DB 2; Length 247;
Best Local Similarity 38.2%; Pred. No. 4.6e-19;
Matches 94; Conservative 33; Mismatches 105; Indels 14; Gaps 8;

Qy 5 VSFSTKATYTITVNFLELRVKLPKGNHSGIPIILKKCDDEPG-KCFVLVALSNDNGQL 63
||| ||| : : ||| : : ||| : : ||| : : ||| : : ||| : : ||| :
Db 2 VSPFLSGATSSSYGVFIENLRKALPYERKLVDPLRLSTL--PGSQRYALIHLTNYADET 59
||| ||| : : ||| : : ||| : : ||| : : ||| : : ||| : : ||| :
Qy 64 AEIAIDVTVVVGVOVRNRSYFFPKDA-PDAAVEGLFKNT-IKTRLHFSGSYPSLS-GEK 120
: ||| ||| ||| : : ||| : : ||| : : ||| : : ||| : : ||| :
Db 60 ISVAIDVTNVVMGTRAGDTSYTFNEASATEAKYVFDAKRKVTLPSYGNVERLQTAA 119
: ||| ||| ||| : : ||| : : ||| : : ||| : : ||| : : ||| :
Qy 121 AYRETTDLGIIEPLRGIKKLDENAI DNYKTPTBIASSLLVVIQMVSEAAAREFTFIENQIRNN 180
||| ||| ||| : : ||| : : ||| : : ||| : : ||| : : ||| :
Db 120 KIRENIPGLPALDSAI-----TTLFYNNANSAASALMWLIQSTSEAAARYKFIEQQIGKR 174
||| ||| ||| : : ||| : : ||| : : ||| : : ||| : : ||| :
Qy 181 PQQRIRPANNTISLENKGKLSFQIR-TSGANGMFSEAVELERANGKKYYTVTDQ--VK 237
: ||| : ||| ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 175 VDRTFLPSLAIISENSWSALSQTQIASLTNGQPETPVVLINAQNRQVRTITNVDAGVWT 234
||| ||| ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Qy 238 PKIALL 243
|||||
Db 235 SNIALL 240
|||||

RESULT 14

JCS606
karasurin C - Trichosanthes kirilowii var. japonica
N;Contains: Karasurin A
C;Species: Trichosanthes kirilowii var. japonica
C;Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 09-Jul-2004
C;Accession: JCS606; JC5033
R; Mizukami, H.; Iida, K.; Kondo, T.; Ogiwara, Y.
BioJ. Pharm. Bull. 20, 711-713, 1997
A;Title: Cloning and bacterial expression of a gene encoding ribosome-inactivating prote
A;Reference number: JCS606; MUID:97356562; PMID:9212998
A;Accession: JCS606
A;Molecule type: DNA
A;Residues: 1-289 <MLZ>
A;Cross-references: UNIPROT:P24478; UNIPARC:UPI000013394C; DDBJ:AB0000666; NID:92329830;
R;Kondo, T.; Mizukami, H.; Takeda, T.; Ogiwara, Y.
BioJ. Pharm. Bull. 15, 1485-1489, 1996
A;Title: Amino acid sequences and ribosome-inactivating activities of karasurin-B and ka
A;Reference number: JCS032; MUID:97108848; PMID:8951169
A;Accession: JCS033
A>Status: preliminary
A;Molecule type: protein
A;Residues: 22-270 <KON>
A;Cross-references: UNIPARC:UPI0000177P1D
C;Comment: This protein is a ribosome-inactivating protein and exhibit cytotoxic, aborti
C;Comment: This protein belongs to type I ribosomal-inactivating proteins which catalyti
C;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
F;22-270/Product: karasurin C #status predicted <MAC>
F;24-270/Product: karasurin A #status predicted <MAA>

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 10, 2006, 10:39:04 ; Search time 12.9668 Seconds
(without alignments)
254.015 Million cell updates/sec

Title: US-10-717-243-2

Perfect score: 1287

Sequence: 1 GLDVTVSFTKGATYTYNFF.....AVDQVKPKIALLKFDVDPK 251

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 97014 seqs, 13122538 residues

Total number of hits satisfying chosen parameters: 97014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New.*
1: /cgn2_6/ptodata/1/pubpaa/US08 NEW PUB. pep.*
2: /cgn2_6/ptodata/1/pubpaa/US06 NEW PUB. pep.*
3: /cgn2_6/ptodata/1/pubpaa/US07 NEW PUB. pep.*
4: /cgn2_6/ptodata/1/pubpaa/PCT NEW PUB. pep.*
5: /cgn2_6/ptodata/1/pubpaa/US03 NEW PUB. pep.*
6: /cgn2_6/ptodata/1/pubpaa/US10 NEW PUB. pep.*
7: /cgn2_6/ptodata/1/pubpaa/US11 NEW PUB. pep.*
8: /cgn2_6/ptodata/1/pubpaa/US60 NEW PUB. pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	343	26.7	268	7 US-11-010-795-24	Sequence 24, Appl
2	343	26.7	576	6 US-10-923-022-1	Sequence 1, Appli
3	343	26.7	630	6 US-10-893-584-274	Sequence 274, App
4	325	25.3	313	7 US-11-010-795-20	Sequence 20, Appl
5	307	23.9	267	6 US-10-517-707A-1	Sequence 1, Appli
6	246.5	19.2	190	6 US-10-923-022-11	Sequence 11, Appl
7	245.5	19.1	200	6 US-10-923-022-10	Sequence 10, Appl
8	243.5	18.9	188	6 US-10-923-022-4	Sequence 4, Appli
9	243.5	18.9	188	6 US-10-923-022-8	Sequence 8, Appli
10	243.5	18.9	189	6 US-10-923-022-6	Sequence 6, Appli
11	242.5	18.8	198	6 US-10-923-022-3	Sequence 3, Appli
12	242.5	18.8	198	6 US-10-923-022-7	Sequence 7, Appli
13	242.5	18.8	199	6 US-10-923-022-5	Sequence 5, Appli
14	240	18.6	267	6 US-10-517-707A-7	Sequence 7, Appli
15	239	18.6	185	6 US-10-923-022-9	Sequence 9, Appli
16	202	15.7	310	7 US-11-010-795-22	Sequence 22, Appl
17	173.5	13.5	179	6 US-10-923-022-2	Sequence 2, Appli
18	83.5	6.5	315	7 US-11-010-795-28	Sequence 28, Appl
19	83	6.4	319	7 US-11-010-795-26	Sequence 26, Appl
20	82.5	6.4	1183	7 US-11-115-639-13	Sequence 13, Appl
21	82.5	6.4	1183	7 US-11-115-639-14	Sequence 14, Appl
22	82.5	6.4	1183	7 US-11-115-639-15	Sequence 15, Appl
23	82.5	6.4	1183	7 US-11-115-639-16	Sequence 16, Appl
24	82.5	6.4	1183	7 US-11-115-639-17	Sequence 17, Appl
25	82.5	6.4	1183	7 US-11-115-639-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1

US-11-010-795-24 365 7 US-11-102-978-9 Sequence 9, Appli
26 80.5 6.3 365 7 US-11-080-991-78 Sequence 78, Appl
27 80.5 6.3 459 6 US-10-453-372-1044 Sequence 1044, Ap
28 79 6.1 459 6 US-11-188-743-19 Sequence 19, Appl
29 79 6.1 934 7 US-11-183-294-20 Sequence 20, Appl
30 79 6.1 934 7 US-10-793-626-3014 Sequence 3014, Ap
31 78 6.1 377 6 US-11-022-562-229 Sequence 229, App
32 77 6.0 386 6 US-10-873-372-1012 Sequence 191, App
33 77 6.0 951 6 US-10-453-372-1012 Sequence 1012, Ap
34 76.5 5.9 417 6 US-10-995-561-791 Sequence 791, App
35 76.5 5.9 417 7 US-11-110-851-61 Sequence 61, Appl
36 76.5 5.9 902 7 US-11-098-686-11082 Sequence 11082, A
37 76.5 5.9 1088 7 US-11-098-686-10718 Sequence 10718, A
38 76.5 5.9 459 6 US-10-453-372-1018 Sequence 1018, Ap
39 76 5.9 459 6 US-10-453-372-1046 Sequence 1046, Ap
40 76 5.9 459 6 US-10-453-372-1048 Sequence 1048, Ap
41 76 5.9 459 6 US-10-453-372-1050 Sequence 1050, Ap
42 76 5.9 483 7 US-11-052-554A-107 Sequence 107, App
43 76 5.9 947 6 US-10-453-372-1010 Sequence 1010, Ap
44 76 5.9 962 6 US-10-453-372-1042 Sequence 1042, Ap
45

US-11-010-795-24
; Sequence 24, Application US/11010795
; Publication No. US20060005271A1
; GENERAL INFORMATION:
; APPLICANT: TUMER, NILGUN E.
; APPLICANT: DI, RONG
; TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING L3 DELTA PROTEINS ARE
; TITLE OF INVENTION: RESISTANT TO TRICHOECENE FUNGAL TOXINS
; FILE REFERENCE: OCIRS 3.0-085
; CURRENT APPLICATION NUMBER: US/11/010,795
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: 60/529,348
; PRIOR FILING DATE: 2003-12-12
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patent in Ver. 3.3
; SEQ ID NO 24
; LENGTH: 268
; TYPE: PRT
; ORGANISM: Ricinus communis
US-11-010-795-24

Query Match 26.7%; Score 343; DB 7; Length 268;
Best Local Similarity 36.8%; Pred. No. 4.8e-25;
Matches 93; Conservative 45; Mismatches 99; Indels 16; Gaps 9;
Qy 5 VSFSTKGNATYTYNFFLNELRVKLKPEGN-SHGIPLLRKKCCDDP-GKCFVLVALSNDNGQ 62
Db 10 INFTTAGATVQSYTNFPIRAVRGLTTGADVRHEIPVLPNVRVGLPNIQRFILVLSNHAEL 69
Qy 63 LAETAIDVTYSVYGVGYOVNRSYFFKADPD-----AAVEGLFKNTIKTR--LHFGGSYPS 115
Db 70 SVTLALDVTNAYVGYRAGNSAYFFH--PDNQEDAEALTHLFTD-VQRYTFAGGNYDR 126
Qy 116 LEGEKA-YRETTDGIIEPLRIGIKKLDENAIIDNYKPTBIASLLVVIQWVSEAAFTPIE 174
Db 127 LEQLAGNLRENIELGNGLPEBAISALYYSTGTQPLTLARSPFICIQMSEARFQVIE 186
Qy 175 NQIRN--NFQORIRPANNTISLENKWKLSQIRTSANGHMFSEAVELERANGKYYVTA 232
Db 187 GEMTRIRYNRSAPDPSPVITLNSWGLSLTAIQESN--QGAPASPIQLQRNGSKFSYVD 245
Qy 233 VDQVKPKIALKPF 245
Db 246 VSILPIIALVMY 258

RESULT 2


```
US-10-923-022-1
; Sequence 1, Application US/10923022
; Publication No. US20060009619A1
; GENERAL INFORMATION:
; APPLICANT: Millard, Mark A
; APPLICANT: Olson, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452U0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/923,022
; CURRENT FILING DATE: 2004-08-23
; PRIOR APPLICATION NUMBER: US/10/083,336
; PRIOR FILING DATE: 2002-02-27
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 576
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-923-022-1

Query Match      26.7%; Score 343; DB 6; Length 576;
Best Local Similarity 36.8%; Pred. No. 1.4e-24;
Matches 93; Conservative 45; Mismatches 99; Indels 16; Gaps 9;

QY 5 VSFSTKGATYTYVNFNLRLVRLKPEGN-SHGIPLLRKKDDP-GKCFVLVALSNDNGQ 62
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
44 INFMTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNVRGLPINQRFILVELSNHAE 103
QY 63 LABIAIDVTSVVVGVGVNRSYFFKADP-----AAVEGLFKNTIKTR--LHFGGSYPS 115
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
104 SVTLALDVNTAVVGYRAGNSAYFFH--PDNQEDAEATHLFTD-VQNYRTAFGCGNYDR 160
QY 116 LEGEKA-YRETTDLGIEPLRIGIKKLDENADINDYKPTIEASSLLVVIQVSEAAARFTPIE 174
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
161 LEQLAGNLRNIELGNGPLEEASALYYSTGGTQPLTLARSFFICIQWISEAARFQVIE 220
QY 175 NQIRN--NFQORIRPANNITISLENKWKLSFOIRTSGANGMPSEAVELERANGKYYVTA 232
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
221 GEMTRIRYNRSAPDPSPVITLNSWGRLSTAIOESN-QGAFASPIQLQRRNGSKFSYVD 279
QY 233 VDQVKPKIALLKPF 245
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
280 VSILIPIALMVI 292

RESULT 3
US-10-893-584-274
; Sequence 274, Application US/10893584
; Publication No. US2005027048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Putac, Adair
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US/0551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US/0403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 274
; LENGTH: 630
; TYPE: PRT
; ORGANISM: Artificial Sequence

US-10-010-795-20
; Sequence 20, Application US/11010795
; Publication No. US20060005271A1
; GENERAL INFORMATION:
; APPLICANT: TUMER, NILGUN E.
; TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING L3 DELTA PROTEINS ARE
; FILE REFERENCE: OCIRS 3.0-085
; CURRENT APPLICATION NUMBER: US/11/010,795
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: 60/529,348
; PRIOR FILING DATE: 2003-12-12
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patent In Ver. 3.3
; SEQ ID NO 20
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Phytolacca americana
US-11-010-795-20

Query Match      25.3%; Score 325; DB 7; Length 313;
Best Local Similarity 31.6%; Pred. No. 3e-23;
Matches 84; Conservative 49; Mismatches 101; Indels 32; Gaps 8;

QY 2 LDTVSPSTKGATYTYVNFNLRLVRLK-PEGNSHGIPLLRKKDDPCKCFVLVALSNDN 60
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
23 VNTIYVNGVSTTISKYATFLNDRLEAKDPSLKCYPMLPNTNTNPK--YVLVELQGSN 80
QY 61 GOLABIAIDVTSVVVGVGVNRSYFFKADP-----VRNRSYFFKD-----APDAAYEGLFKNT 102
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
81 KKTITLMLRRNNLVYMGYSDFETNKCXYHIFNDISGTERQDVETTLCPNA-----NSR 134
QY 103 IKTRLHFGGSYPSLEGEKAY--RETTDLGIEPLRIGIKKLDENADINDYKPTIEASSLLV 160
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
135 VSKNINPDSRYPTLESKAGVRSQVQLGIQILDNSNICKI--SGVMSFTEKTEAEFLVLA 192
QY 161 IQMUSEAARFTPIENQIRNRFQORIRPANNITISLENKWKLSFOIRTSGANGMPSEAVEL 220
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
193 IQMUSEAARFKYIENQVKTNFRNFRNPNKVLNQLQETWGIKSTATH-DAKNGVLPPKLEL 251
QY 221 ERANGKYYVTVAVDQVKPKIALLKPFV 246
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
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Db 252 VDASGAKWILVRDEIKPDVALLNV 277

RESULT 5

US-10-517-707A-1

; Sequence 1, Application US/10517707A
; Publication No. US20060019885A1
; GENERAL INFORMATION:
; APPLICANT: BAKER, Matthew
; APPLICANT: CARE, Francis J.
; TITLE OF INVENTION: MODIFIED BRYODIN 1 WITH REDUCED
; TITLE OF INVENTION: IMMUNOGENICITY
; FILE REFERENCE: MER-134
; CURRENT APPLICATION NUMBER: US/10/517,707A
; PRIOR FILING DATE: 2004-12-10
; PRIOR APPLICATION NUMBER: PCT/EP03/06055
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: EP 02012911.0
; PRIOR FILING DATE: 2002-08-11
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-517-707A-1

Query Match 23.9%; Score 307; DB 6; Length 267;
Best Local Similarity 36.3%; Pred. No. 1.2e-21;
Matches 89; Conservative 36; Mismatches 108; Indels 12; Gaps 7;
QY 5 VSPSTKGATYTYVNFNLRLVRLKPEGNHGIPLLRKKDDPGKCFVLVALSNDNGOLA 64
DB 2 VSPFLSGATTSYGVFIKNLREALPVRKVYVNIPLRSSISGSR-YTLHLHTYADETI 60
QY 65 EIAIDVTSVYVGVQVNRNSYFFKDA-PDAAYEGLFKNT-INTRLHFGSGYPSLE-GEKA 121
DB 61 SVADVNTVNYINGYLADGVSYFFNEASATAAKVFFKDAKKKVTLPYSGNYERLQTAAGK 120
QY 122 YRETTDLGIEPLRIGIKKLDENAIQKPTETASLLVVIQMVSEARFTPIENQIRNF 181
DB 121 IRENTPLGLPALDSAI-----TTLTYTASSAALLVLIQSTAESARYKFTIQGKRV 175
QY 182 QORIRPANNITSLNKGKLSQIR-TSGANGMFSEAVELEERANGKTYVT--AVDQVKP 238
DB 176 DKTEPLSLATISLNNWSALSQIQIASTNNGQFSPVVLIDGNNQVSIITNASARVTS 235
QY 239 KIALL 243
DB 236 NIALL 240

RESULT 6

US-10-923-022-11

; Sequence 11, Application US/10923022
; Publication No. US20060009619A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/923,022
; CURRENT FILING DATE: 2004-08-23
; PRIOR APPLICATION NUMBER: US/10/083,336
; PRIOR FILING DATE: 2002-02-27
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Ricinus communis

US-10-923-022-11

Query Match 19.2%; Score 246.5; DB 6; Length 190;
Best Local Similarity 35.4%; Pred. No. 3.5e-16;
Matches 68; Conservative 32; Mismatches 73; Indels 19; Gaps 6;
QY 5 VSPSTKGATYTYVNFNLRLVRLKPEGNHGIPLLRKKDDPGKCFVLVALSNDNGOLA 64
DB 10 INFTTAGATVQSYTNFIRAVRGLTLPVNRVGLPINQR-----FILVELSNHAEISV 61
QY 65 EIAIDVTSVYVGVQVNRNSYFFKDA-PD-----RAYEGLFKNTIKTR--LHFGSGYPSLE 117
DB 62 TLALDVTNAYVVGVRAGNSAYFFH--PDNQDEAEAITHLFTD-VQNRVTFAPGGNYDRLE 118
QY 118 GEKA-YRETTDLGIEPLRIGIKKLDENAIQKPTETASLLVVIQMVSEARFTPIENQ 176
DB 119 QLAGNLRENIELNGPLLEASALYYSTGTQPLTLARSFTIICMISEARFOYIERGE 178
QY 177 IRNNFQQRIRPA 188
DB 179 MRTRIRYNRRA 190

RESULT 7

US-10-923-022-10

; Sequence 10, Application US/10923022
; Publication No. US20060009619A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/923,022
; CURRENT FILING DATE: 2004-08-23
; PRIOR APPLICATION NUMBER: US/10/083,336
; PRIOR FILING DATE: 2002-02-27
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Ricinus communis

US-10-923-022-10

Query Match 19.1%; Score 245.5; DB 6; Length 200;
Best Local Similarity 36.1%; Pred. No. 4.7e-16;
Matches 70; Conservative 32; Mismatches 79; Indels 13; Gaps 7;
QY 5 VSPSTKGATYTYVNFNLRLVRLKPEGN-SHGIPLLRKKDDP-GKCFVLVALSNDNGQ 62
DB 10 INFTTAGATVQSYTNFIRAVRGLTTGADVREHFPVLPNRVGLPINQRFILVELSNHAE 69
QY 63 LAEIAIDVTSVYVGVQVNRNSYFFKDA-PD-----AAYEGLFKNTIKTR--LHFGSGYPS 115
DB 70 SVTLALDVTNAYVVGVRAGNSAYFFH--PDNQDEAEAITHLFTD-VQNRVTFAPGGNYDR 126
QY 116 LEGEKA-YRETTDLGIEPLRIGIKKLDENAIQKPTETASLLVVIQMVSEARFTPIE 174
DB 127 LEQLAGNLRENIELNGPLLEASALYYSTGTQPLTLARSFTIICMISEARFOYIER 186
QY 175 NOIRNNFQQRIRPA 188
DB 187 GEMTRIRYNRRA 200

RESULT 8

US-10-923-022-4

; Sequence 4, Application US/10923022
; Publication No. US20060009619A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A


```
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/923,022
; CURRENT FILING DATE: 2004-08-23
; PRIOR APPLICATION NUMBER: US/10/083,336
; PRIOR FILING DATE: 2002-02-27
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 4
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-923-022-4

Query Match      18.9%; Score 243.5; DB 6; Length 188;
Best Local Similarity 36.3%; Pred. No. 6.6e-16;
Matches 69; Conservative 31; Mismatches 67; Indels 23; Gaps 7;

QY 5 VSFSTKGATYTYVNFNLNLRVKKPEGNSHGIPILRRKCCDDPGKCFVLVALSNDNGQLA 64
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 9 INFTTAGATVQSYTNFIRAVRGLTVLPNRVGLPINQR-----FILVELSNHAELSV 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 65 ETAIDVTSVYVVGQVRNRSYFFKDAPD-----AAEGLFKNTIKTR--LHFGGSYPSLE 117
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 TLALDVTNAYVVGVRAGNSAYFFH--PDNQEDAEAIHTLFTD-VQNRVTFAGGNYDRLE 117
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 118 GEKA-YRETTDLGIEPLRIGIKKLDENAIQKPEIASSLLVWQVSEARFTFIENQ 176
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db - 118 QLAGNLRNIELGNGPLEEASALYYSTGGTQTLPTLARSFIICQMISEARFOYIEGE 177
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 177 IRNNFQQRIR 186
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 178 MRT-----RIR 183
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 9
US-10-923-022-8
; Sequence 8, Application US/10923022
; Publication No. US20060009619A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/923,022
; CURRENT FILING DATE: 2004-08-23
; PRIOR APPLICATION NUMBER: US/10/083,336
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 8
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-923-022-8

Query Match      18.9%; Score 243.5; DB 6; Length 188;
Best Local Similarity 36.3%; Pred. No. 6.6e-16;
Matches 69; Conservative 31; Mismatches 67; Indels 23; Gaps 7;

QY 5 VSFSTKGATYTYVNFNLNLRVKKPEGNSHGIPILRRKCCDDPGKCFVLVALSNDNGQLA 64
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 9 INFTTAGATVQSYTNFIRAVRGLTVLPNRVGLPINQR-----FILVELSNHAELSV 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 65 ETAIDVTSVYVVGQVRNRSYFFKDAPD-----AAEGLFKNTIKTR--LHFGGSYPSLE 117
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 TLALDVTNAYVVGVRAGNSAYFFH--PDNQEDAEAIHTLFTD-VQNRVTFAGGNYDRLE 117
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 118 GEKA-YRETTDLGIEPLRIGIKKLDENAIQKPEIASSLLVWQVSEARFTFIENQ 176
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db - 118 QLAGNLRNIELGNGPLEEASALYYSTGGTQTLPTLARSFIICQMISEARFOYIEGE 177
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 177 IRNNFQQRIR 186
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 178 MRT-----RIR 183
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 11
US-10-923-022-3
; Sequence 3, Application US/10923022
; Publication No. US20060009619A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/923,022
; CURRENT FILING DATE: 2004-08-23
; PRIOR APPLICATION NUMBER: US/10/083,336
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-923-022-3

Query Match      18.9%; Score 243.5; DB 6; Length 189;
Best Local Similarity 36.3%; Pred. No. 6.6e-16;
Matches 69; Conservative 31; Mismatches 67; Indels 23; Gaps 7;

QY 5 VSFSTKGATYTYVNFNLNLRVKKPEGNSHGIPILRRKCCDDPGKCFVLVALSNDNGQLA 64
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 10 INFTTAGATVQSYTNFIRAVRGLTVLPNRVGLPINQR-----FILVELSNHAELSV 61
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 65 ETAIDVTSVYVVGQVRNRSYFFKDAPD-----AAEGLFKNTIKTR--LHFGGSYPSLE 117
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 62 TLALDVTNAYVVGVRAGNSAYFFH--PDNQEDAEAIHTLFTD-VQNRVTFAGGNYDRLE 118
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 118 GEKA-YRETTDLGIEPLRIGIKKLDENAIQKPEIASSLLVWQVSEARFTFIENQ 176
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 119 QLAGNLRNIELGNGPLEEASALYYSTGGTQTLPTLARSFIICQMISEARFOYIEGE 178
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 177 IRNNFQQRIR 186
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 179 MRT-----RIR 184
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 11
US-10-923-022-3
; Sequence 3, Application US/10923022
; Publication No. US20060009619A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/923,022
; CURRENT FILING DATE: 2004-08-23
; PRIOR APPLICATION NUMBER: US/10/083,336
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-923-022-3
```



```
; ORGANISM: Ricinus communis
US-10-923-022-3

Query Match      18.8%; Score 242.5; DB 6; Length 198;
Best Local Similarity 37.0%; Pred. No. 8.9e-16;
Matches 71; Conservative 31; Mismatches 73; Indels 17; Gaps 8;

QY 5 VSPSTKGATYTYVNFNLRLVKKPEGN-SHGIPLLRKKCDP-GKCFVLVALSNDNGQ 62
DB 9 INFTAGATVQSYTNFIRAVRGLTTGADVREHPIVLPNVRVGLPNQRFILVELSNHAE 68
QY 63 LAEIAIDVTSVYVGVQVNRNSYFFKADP-----AAYEGLFKNTIKTR--LHFGGSYPS 115
DB 69 SVTLALDVNAYVVGVRAGNSAYFFH--PDNQEDAEATHLFTD-VQNYTFAFGNYDR 125
QY 116 LEGEKA-YRETTDLGIEPLRIGIKKLDENADINYPTEIASLLVVIQMVSEAAARPTFIE 174
DB 126 LEQLAGNLRENIELGNGLPELEAISALYYSTGGTQPLTARSFIICQWISAAARFQYIE 185
QY 175 NOIRNNFOQIR 186
DB 186 GEMRT----RIR 193

RESULT 12
US-10-923-022-7
; Sequence 7, Application US/10923022
; Publication No. US20060009619A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/923,022
; CURRENT FILING DATE: 2004-08-23
; PRIOR APPLICATION NUMBER: US/10/083,336
; PRIOR FILING DATE: 2002-02-27
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-923-022-7

Query Match      18.8%; Score 242.5; DB 6; Length 198;
Best Local Similarity 37.0%; Pred. No. 8.9e-16;
Matches 71; Conservative 31; Mismatches 73; Indels 17; Gaps 8;

QY 5 VSPSTKGATYTYVNFNLRLVKKPEGN-SHGIPLLRKKCDP-GKCFVLVALSNDNGQ 62
DB 9 INFTAGATVQSYTNFIRAVRGLTTGADVREHPIVLPNVRVGLPNQRFILVELSNHAE 68
QY 63 LAEIAIDVTSVYVGVQVNRNSYFFKADP-----AAYEGLFKNTIKTR--LHFGGSYPS 115
DB 69 SVTLALDVNAYVVGVRAGNSAYFFH--PDNQEDAEATHLFTD-VQNYTFAFGNYDR 125
QY 116 LEGEKA-YRETTDLGIEPLRIGIKKLDENADINYPTEIASLLVVIQMVSEAAARPTFIE 174
DB 126 LEQLAGNLRENIELGNGLPELEAISALYYSTGGTQPLTARSFIICQWISAAARFQYIE 185
QY 175 NOIRNNFOQIR 186
DB 186 GEMRT----RIR 193

RESULT 13
US-10-923-022-5
; Sequence 5, Application US/10923022
; Publication No. US20060009619A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/923,022
; CURRENT FILING DATE: 2004-08-23
; PRIOR APPLICATION NUMBER: US/10/083,336
; PRIOR FILING DATE: 2002-02-27
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-923-022-5

Query Match      18.8%; Score 242.5; DB 6; Length 199;
Best Local Similarity 37.0%; Pred. No. 8.9e-16;
Matches 71; Conservative 31; Mismatches 73; Indels 17; Gaps 8;

QY 5 VSPSTKGATYTYVNFNLRLVKKPEGN-SHGIPLLRKKCDP-GKCFVLVALSNDNGQ 62
DB 10 INFTAGATVQSYTNFIRAVRGLTTGADVREHPIVLPNVRVGLPNQRFILVELSNHAE 69
QY 63 LAEIAIDVTSVYVGVQVNRNSYFFKADP-----AAYEGLFKNTIKTR--LHFGGSYPS 115
DB 70 SVTLALDVNAYVVGVRAGNSAYFFH--PDNQEDAEATHLFTD-VQNYTFAFGNYDR 126
QY 116 LEGEKA-YRETTDLGIEPLRIGIKKLDENADINYPTEIASLLVVIQMVSEAAARPTFIE 174
DB 127 LEQLAGNLRENIELGNGLPELEAISALYYSTGGTQPLTARSFIICQWISAAARFQYIE 186
QY 175 NOIRNNFOQIR 186
DB 187 GEMRT----RIR 194

RESULT 14
US-10-517-707A-7
; Sequence 7, Application US/10517707A
; Publication No. US20060019885A1
; GENERAL INFORMATION:
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis J.
; TITLE OF INVENTION: MODIFIED BRYODIN 1 WITH REDUCED
; FILE REFERENCE: MER-134
; CURRENT APPLICATION NUMBER: US/10/517,707A
; CURRENT FILING DATE: 2004-12-10
; PRIOR APPLICATION NUMBER: PCT/EP03/06055
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: EP 02012911.0
; PRIOR FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Modified byrodin 1 protein
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 48, 49, 51, 54
; OTHER INFORMATION: Xaa=Ala, Gly, Pro
; OTHER INFORMATION: Xaa=Met, Ala, Gly, Pro, Ile
; OTHER INFORMATION: Xaa=Ala, Gly, Pro
; OTHER INFORMATION: Xaa=Pro, Tyr
; FEATURES:
; NAME/KEY: VARIANT
; LOCATION: 55, 60, 64, 66
```



```

; OTHER INFORMATION: Xaa=Thr, Ser
; OTHER INFORMATION: Xaa=Pro
; OTHER INFORMATION: Xaa=Ala, Gly, Pro
; OTHER INFORMATION: Xaa=Ala, Gly, Pro
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 94, 95, 103, 114
; OTHER INFORMATION: Xaa=Ala, Gly, Pro, His, Asp, Glu, Asn, Gln, Lys,
; OTHER INFORMATION: Arg, Ser, Thr
; OTHER INFORMATION: Xaa=Ala, Gly, Pro
; OTHER INFORMATION: Xaa=Ala, Gly, Pro
; OTHER INFORMATION: Xaa=Ala, Pro, Ser, Thr, His, Lys
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 117, 119, 120, 121
; OTHER INFORMATION: Xaa=Thr
; OTHER INFORMATION: Xaa=His
; OTHER INFORMATION: Xaa=Ser
; OTHER INFORMATION: Xaa=Ala, Ser, thr, Pro, Asn, Asp, Glu, Gly, His,
; OTHER INFORMATION: Lys, Gln
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 122, 125, 139, 132
; OTHER INFORMATION: Xaa=Thr
; OTHER INFORMATION: Xaa=Ala, Pro
; OTHER INFORMATION: Xaa=Ala, Ile, Phe, Gly, Met, Pro, Val, Trp, Tyr
; OTHER INFORMATION: Xaa=Phe, Pro, Trp
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (137)...(143)
; OTHER INFORMATION: Xaa=Ala, Gly, Pro
; OTHER INFORMATION: Xaa=Ala, Gly, Pro
; OTHER INFORMATION: Xaa=Ala, Gly, Pro
; OTHER INFORMATION: Xaa=Ala, Gly, Pro
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (152)...(155)
; OTHER INFORMATION: Xaa=Ala, Gly, Pro, Ser, Thr
; OTHER INFORMATION: Xaa=Ala, Gly, Pro, Ile, Met, Ser, Thr
; OTHER INFORMATION: Xaa=Ala, Gly, Pro
; OTHER INFORMATION: Xaa=Ala, Gly, Pro, Ser, Thr, His, Asp, Asn, Gln,
; OTHER INFORMATION: Lys, Arg
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (187)...(198)
; OTHER INFORMATION: Xaa=Ala, Gly, Pro, Thr, Ser, His, Lys, Arg, Asp,
; OTHER INFORMATION: Glu, Asn, Gln
; OTHER INFORMATION: Xaa=Ala, Gly, Pro, Thr, Ser, His, Lys, Arg, Asp,
; OTHER INFORMATION: Glu, Asn, Gln
; OTHER INFORMATION: Xaa=Gln
; OTHER INFORMATION: Xaa=His, Lys, Arg, Asp, Glu, Asn,, Phe, Leu, Pro,
; OTHER INFORMATION: Ser, Tyr, Trp
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (200)...(202)
; OTHER INFORMATION: Xaa=Ala, Gly, Pro, Thr, Ser, His, Lys, Arg, Asp,
; OTHER INFORMATION: Glu, Asn, Gln
; OTHER INFORMATION: Xaa=Asp
US-10-517-707A-7

Query Match      18.6%; Score 240; DB 6; Length 267;
Best Local Similarity 30.5%; Pred.No. 2.3e-15;
Matches 75; Conservative 33; Mismatches 124; Indels 14; Gaps 7;

QY 5 VSFSTKGATITTYVNFMLNLRVVKLPKPGNSHGIPLLRKKDDPGKCFVLVALSNDNGOLA 64
Db 2 VSFRLSGATTTSYGVPKLNRLALPYERKYNVPIPLRSISGSR-YXXLXLTXXADETX 60

QY 65 EIAIDVTSVYVGVQVRNRSYFFKDA-PDAAYEGLFKNT-INKRLHFGSGSYPSLEGEKAY 122
Db 61 SVAXDKTNVYINGYLADGVSYFNEASATEAKKXFKDAKKKXLTLPYSGNY-----ERX 114

QY 123 RETTDLGIEPLRIGIKLDENADINVKPT--EIASLLVVIQMVSEAAARFTFIENQIRNN 180

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Db 115 QTXAXXXENYPLGXPADSDAXITTYXXXTASASASAXXXIXQTAESARYKFEQQIGKR 174
QY 181 FQORIRPANNTISLENKWKLSFQIRTSGA-NGMFSEAVELELANGKKYYVT--AVDQVK 237
Db 175 VDKTFLPSLATKXSNENWSAXSXQXASTNNGQFSPVVLIDGNQORVSITNASARVVT 234
QY 238 PKIALL 243
Db 235 SNIAL 240

RESULT 15
US-10-923-022-9
; Sequence 9, Application US/10923022
; Publication No. US20060009619A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrnes, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/923,022
; CURRENT FILING DATE: 2004-08-23
; PRIOR APPLICATION NUMBER: US/10/083,336
; PRIOR FILING DATE: 2002-02-27
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-923-022-9

Query Match      18.6%; Score 239; DB 6; Length 185;
Best Local Similarity 36.3%; Pred.No. 1.7e-15;
Matches 69; Conservative 31; Mismatches 64; Indels 26; Gaps 8;

QY 5 VSFSTKGATITTYVNFMLNLRVVKLPKPGNSHGIPLLRKKDDPGKCFVLVALSNDNGOLA 64
Db 9 INFTTAGATVQSYTNFIRAVGRLT---NRVGLPINQR-----FILVELSNHAELSV 57

QY 65 EIAIDVTSVYVGVQVRNRSYFFKDA-PDAAYEGLFKNTIKTR--LHFGGSYPSLE 117
Db 58 TLALDVTNAYVGVYRAGNSAYFFH--PDNQBDAAEAITHLFTD-VQNRVYTPAFGGNYDRLE 114

QY 118 GEKA-YRETTDLGIEPLRIGIKLDENADINVKPT-EIASLLVVIQMVSEAAARFTFIENQ 176
Db 115 QLQNLRENIELNGPLEEALISALYYSTGTGTLPTLARSFICTQMISEAARFQYIEGE 174

QY 177 IRNNFQQRIR 186
Db 175 MRT----RIR 180

```

Search completed: February 10, 2006, 10:45:19
Job time : 13.9668 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 10, 2006, 09:56:49 ; Search time 10.8856 Seconds
(without alignments)
807.265 Million cell updates/sec

Title: US-10-717-243-56

Perfect score: 114

Sequence: 1 CHHNSRVARWASDEFFSMC 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_21.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	114	100.0	20	2 AAR37300	Aar37300 E.coli sh
2	114	100.0	293	2 AAW58827	Aaw58827 Shiga tox
3	114	100.0	293	2 AAY39393	Aay39393 Shiga-lik
4	114	100.0	293	3 AAY69046	Aay69046 Amino aci
5	114	100.0	315	2 AAW06403	Aaw06403 Verotoxig
6	114	100.0	315	2 AAW21702	Aaw21702 Shiga-lik
7	114	100.0	315	2 AAW25139	Aaw25139 SLT-1 (a
8	114	100.0	315	3 AAY96681	Aay96681 E. coli v
9	114	100.0	315	5 AAY77817	Aay77817 E. coli v
10	114	100.0	315	7 ADC00545	Adc00545 Enterohae
11	114	100.0	315	7 ADH34319	Adh34319 Verotoxin
12	114	100.0	316	2 AAW25786	Aaw25786 Phage H19
13	114	100.0	323	2 AAW06407	Aaw06407 Histidine
14	114	100.0	323	3 AAY96686	Aay96686 Recombina
15	114	100.0	323	5 AAY77822	Aay77822 HIS-tagge
16	114	100.0	326	2 AAW06413	Aaw06413 Flag tag/
17	114	100.0	326	5 AAY96692	Aay96692 FLAG tag/
18	114	100.0	326	5 AAY77828	Aay77828 Flag tag/
19	114	100.0	332	2 AAW29294	Aaw29294 BPI pepti
20	114	100.0	409	2 AAR13118	Aar13118 Shiga-lik
21	114	100.0	409	2 AAY55891	Aay55891 E.coli ba
22	114	100.0	409	3 AAY78591	Aay78591 E. coli b
23	114	100.0	690	3 AAY96694	Aay96694 MBP-VT-1
24	114	100.0	690	5 AAY77830	Aay77830 MBPNVTI-A

25	114	100.0	708	2 AAW06411	Aaw06411 Maltose b
26	114	100.0	708	3 AAY96690	Aay96690 MBP-VT-1
27	114	100.0	708	5 AAU77826	Aau77826 MBPNVTI-A
28	51	44.7	17	9 ADZ89477	Adz89477 Substrate
29	47	41.2	135	7 ADJ68214	Adj68214 Human hea
30	46	40.4	18	9 ADZ89463	Adz89463 Substrate
31	46	40.4	35	7 ADE95989	Ade95989 Human uri
32	46	40.4	35	7 ADK14898	Adk14898 Urinary s
33	46	40.4	196	6 ABU38500	Abu38500 Protein e
34	46	40.4	204	7 ABO69919	Abo69919 Pseudomon
35	45	39.5	19	7 ABR82617	Abr82617 P. aerugi
36	45	39.5	386	3 AAG59236	Agg59236 Arabidops
37	45	39.5	413	6 ADA34573	Ada34573 Acinetoba
38	45	39.5	525	7 ABO79520	Abo79520 Pseudomon
39	44.5	39.0	250	8 ADS21292	Ads21292 Bacterial
40	44.5	39.0	280	8 ADX90199	Adx90199 Plant ful
41	44.5	39.0	544	3 AAB53464	Aab53464 Human col
42	44	38.6	137	4 AAM79060	Aam79060 Human pro
43	44	38.6	137	2 ADJ69294	Adj69294 Human hea
44	44	38.6	138	2 AAW60837	Aaw60837 Human SQM
45	44	38.6	138	5 ABG72567	Abg72567 Human cel

ALIGNMENTS

RESULT 1
AAR37300
ID AAR37300 standard; protein; 20 AA.
XX
AC AAR37300;
XX
DT 25-MAR-2003 (revised)
DT 13-SEP-1993 (first entry)
XX
DE E.coli shiga-like toxin segment.
XX
KW Type I ribosome-inactivating protein; ricin; momordin; immunoconjugate;
KW autoimmune disease; cell killing; toxin; human engineered antibody;
KW variable region; light chain; cell targeting; chimeric antibody; SLT.
OS Escherichia coli.
FH Key Location/Qualifiers
FT Disulfide-bond 1..20
FT /note= "intervening loop includes protease sensitive
FT amino acid sequence"
XX
PN MO9309130-A1.
XX
PD 13-MAY-1993.
XX
PF 04-NOV-1992; 92WO-US009487.
XX
PR 04-NOV-1991; 91US-00787567.
PR 19-JUN-1992; 92US-00901707.
XX
PA (XOMA) XOMA CORP.
XX
PI Bernhard SL, Better MD, Carroll SF, Lane JA, Lei SP;
XX WPI; 1993-167617/20.
XX
PT Analogues of type I ribosome inactivating protein - useful as cytotoxic
PT agents, immuno toxins for treating auto immune diseases, cancer, graft
XX versus host disease and selective cell killing insvivo.
XX
PS Example 10; Page 114; 163pp; English.
XX
CC The invention covers analogues of the plant type I RIP gelonin which have
CC a non-naturally occurring Cys residue in a position which enables the
CC analogue to be conjugated via a disulphide linkage to a molecule which
CC specifically binds to a target cell. Pref. target-cell binding molecules

CC are antibodies or their fragments, esp. human engineered H65 antibody
 CC fragments. Fusion constructs were assembled that included a natural
 CC sequence gelonin gene fused to an H65 truncated heavy chain gene or an
 CC H65 light chain (kappa) gene. A DNA linker encoding a peptide segment of
 CC the E.coli shiga-like toxin was inserted between the gelonin gene and the
 CC Ab gene. The resulting immunoconjugates can be used as cytotoxic
 CC therapeutic agents. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 20 AA;

Query Match 100.0%; Score 114; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 5.5e-12;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHHSRVARMASDEFPSSMC 20
 |||||
 DB 1 CHHHSRVARMASDEFPSSMC 20

RESULT 2
 AAW58827
 ID AAW58827 standard; peptide; 293 AA.

AC AAW58827;
 XX

DT 18-AUG-1998 (first entry)

DE Shiga toxin type 1 mature A subunit.

KW Histone-tag; toxoid; antibody; treatment; diagnosis; prevention; Stx;
 KW haemorrhagic colitis; haemolytic uremic syndrome.

OS Shigella dysenteriae.

XX WO9811229-A2.

XX 19-MAR-1998.

PF 09-SEP-1997; 97WO-US015836.

PR 10-SEP-1996; 96US-0025637P.

PA (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.

PI O'Brien AD, Schmitt CK;

XX WPI; 1998-207390/18.

DR N-PSDB; AAV11400.

XX Purification and isolation of histidine-tagged Shiga toxins - useful in
 PT vaccines against haemorrhagic colitis and haemolytic uremic syndrome.

PS Claim 1; Fig 2; 47pp; English.

XX The Shiga toxin (Stx) peptides (AAW58827-W58830) were histidine-tagged to
 CC simplify and expedite purification. Non toxic Shiga toxoids, Fusion
 CC proteins of His-tagged Shiga toxins/toxoids and antibodies can be used in
 CC the treatment, diagnosis or prevention of infections mediated by toxins
 CC of the Stx family. These are associated with haemorrhagic colitis and the
 CC life-threatening sequelae, haemolytic uremic syndrome. Shiga antibodies
 CC are also useful for the treatment, diagnosis and prevention of disease
 CC and infections by pathogenic Escherichia coli

XX Sequence 293 AA;

Query Match 100.0%; Score 114; DB 2; Length 293;
 Best Local Similarity 100.0%; Pred. No. 1e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHHSRVARMASDEFPSSMC 20
 |||||
 DB 242 CHHHSRVARMASDEFPSSMC 261

RESULT 3
 AAY39393
 ID AAY39393 standard; protein; 293 AA.

AC AAY39393;

DT 20-DEC-1999 (first entry)

DE Shiga-like Toxin 1, A subunit.

KW Shiga toxin; ShT; Shiga-like toxin; SLT; A subunit; B subunit; ricin;
 KW microorganism clone; combinatorial library; therapeutic protein;
 KW medicament; target cell; binding specificity.

OS Shigella dysenteriae.

PN WO9940185-A1.

PD 12-AUG-1999.

PF 08-DEC-1998; 98WO-CA001137.

PR 04-FEB-1998; 98CA-02222993.

XX (ONTA-) ONTARIO CANCER INST.

PI Gariepy J, Bray MR;

XX WPI; 1999-590695/50.

XX Production of cytotoxic heteromeric protein combinatorial libraries,
 PT useful for ability to specifically bind to and kill a target cell.

XX Example 1; Fig 1a; 61pp; English.

XX This is the Shiga-like toxin (SLT) subunit A amino acid sequence. SLT is
 CC a bacterial toxin related to the Shiga toxin (ShT). SLT and ShT have the
 CC smallest known B subunit of all AB toxins, and the A subunit has
 CC identical catalytic activity as the corresponding subunit in ricin. The B
 CC subunit (AAY39394) is identical for both ShT and SLT. Both the A and B
 CC subunit amino acid sequences are used in the methods of the invention,
 CC which relates to the creation of a library of microorganism clones
 CC producing mutant proteins which are then screened for their ability to
 CC specifically bind to and kill target cell. AAY39395-Y39389 and AAY3001-
 CC Y43024 are examples of mutant B subunits identified by the methods of the
 CC invention. The B subunit of the toxin has high binding specificity, and
 CC therefore mutant versions of the B subunit may target the toxin to a
 CC specific cell. Cytotoxic mutant proteins identified by the method can be
 CC used to identify therapeutic proteins and medicaments having binding
 CC specificity for a target cell. The cytotoxic mutants can also be used to
 CC construct diagnostic probes for detecting the presence of cell surface
 CC markers. These medicaments can be used to target medicines to target
 CC cells in host organisms

XX Sequence 293 AA;

Query Match 100.0%; Score 114; DB 2; Length 293;
 Best Local Similarity 100.0%; Pred. No. 1e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHHSRVARMASDEFPSSMC 20
 |||||
 DB 242 CHHHSRVARMASDEFPSSMC 261

RESULT 4
 AAY69046
 ID AAY69046 standard; protein; 293 AA.

AC AAY69046;

DT 30-MAY-2000 (first entry)

XX Amino acid sequence of exemplary cell toxin shiga toxin A-chain.
 DE
 XX
 XX Chemokine receptor; ligand; inflammatory response; immune effector cell;
 KW secondary tissue damage; central nervous system injury; shiga;
 KW CNS inflammatory disease; neurodegenerative disorder; heart disease;
 KW inflammatory eye disease; inflammatory bowel disease; PCR primer;
 KW inflammatory joint disease; inflammatory kidney; renal disease;
 KW inflammatory lung disease; inflammatory nasal disease; thyroiditis;
 KW inflammatory thyroid disease; cytokine-regulated cancer; ss.
 XX
 XX Shigella dysenteriae.
 OS
 XX WO200004926-A2.
 FN
 XX
 XX 03-FEB-2000.
 PD
 XX
 XX 21-JUL-1999; 99WO-CA000659.
 PF
 XX
 XX 22-JUL-1998; 98US-00120523.
 PR
 XX
 XX (OSPR-) OSPREY PHARM LTD.
 PA
 XX
 XX McDonald JR, Coggins PJ;
 PI
 XX WPI; 2000-182542/16.
 DR
 XX
 XX A new therapeutic agent comprising a conjugate for treating secondary
 PT tissue damage and other disease conditions like Alzheimer's disease,
 PT stroke, Parkinson's disease and atherosclerosis.
 PT
 XX Disclosure; Page 67; 204pp; English.
 FS
 XX
 XX The present sequence represents an exemplary cell toxin, which can be
 CC incorporated into the conjugates of the invention. The specification
 CC describes a conjugate, comprising a targeted agent and a chemokine
 CC receptor ligand. The conjugate binds to a chemokine receptor resulting in
 CC internalisation of the targeted agent in cells bearing the receptor. The
 CC conjugates are used for formulating a medicament or for treating
 CC disorders associated with inflammatory responses resulting from
 CC activation, proliferation and migration of immune effector cells. The
 CC disorders or disease states comprise secondary tissue damage such as
 CC central nervous system (CNS) injury, CNS inflammatory diseases,
 CC neurodegenerative disorders, heart disease, inflammatory eye diseases,
 CC inflammatory bowel diseases, inflammatory joint diseases, inflammatory
 CC kidney or renal diseases, inflammatory lung diseases, inflammatory nasal
 CC diseases, inflammatory thyroid disease such as thyroiditis, or cytokine-
 CC regulated cancers
 XX
 SQ Sequence 293 AA;
 Query Match 100.0%; Score 114; DB 3; Length 293;
 Best Local Similarity 100.0%; Pred. No. 1e-10; Mismatches 0; Indels 0; Gaps 0;
 Matches 20; Conservative 0;
 Qy 1 CHHHSRVARVASDEFPSC 20
 Db 242 CHHHSRVARVASDEFPSC 261
 RESULT 5
 AA06403
 ID AA06403 standard; protein; 315 AA.
 XX
 AC AA06403;
 XX
 DT 25-FEB-1997 (first entry)
 DE Verotoxinigenic E. coli toxin (VT1) subunit A.
 XX
 XX Verotoxin; Escherichia coli; enteric infection; diarrhoea; vaccine;
 KW haemolytic uraemic syndrome; detection.
 XX

OS Escherichia coli.
 FN WO9630043-A1.
 XX
 PD 03-OCT-1996.
 XX
 PF 25-MAR-1996; 96WO-US004093.
 XX
 PR 24-MAR-1995; 95US-00410058.
 XX
 XX (OPHI-) OPHIDIAN PHARM INC.
 PA
 XX Carroll SB, Stafford DC, Padhye NV;
 PI WPI; 1996-505779/50.
 XX DR N-PSDB; AAT42649.
 DR
 XX Compn. contg. neutralising antitoxin against E.coli vero-toxin - used to
 PT treat intoxicated individuals, and as a prophylactic against diarrhoeal
 PT disease or extra-intestinal complications of E.coli infection.
 XX
 PS Example 6; Page 51; 101pp; English.
 XX
 CC Compositions containing neutralising antitoxin against one or more E.
 CC coli verotoxin (VT) can be used to treat intoxicated adults and children
 CC with enteric bacterial infections. They may also be used as prophylactics
 CC e.g. as a vaccine, against diarrhoeal disease or the development of extra
 CC -intestinal complications of E.coli infection, especially haemolytic
 CC uraemic syndrome. The antitoxin can also be used to detect E. coli VT in
 CC a sample. The VT is recombinant, preferably a fusion protein containing a
 CC non-VT protein sequence and part of the E.coli VT1 or VT2 sequence
 XX
 SQ Sequence 315 AA;
 Query Match 100.0%; Score 114; DB 2; Length 315;
 Best Local Similarity 100.0%; Pred. No. 1e-10; Mismatches 0; Indels 0; Gaps 0;
 Matches 20; Conservative 0;
 Qy 1 CHHHSRVARVASDEFPSC 20
 Db 264 CHHHSRVARVASDEFPSC 283
 RESULT 6
 AA06403
 ID AA06403 standard; protein; 315 AA.
 XX
 AC AA06403;
 XX
 DT 17-OCT-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 26-SEP-1997 (first entry)
 XX
 DE Shiga-like toxin (SLT-1) RIP.
 XX
 KW pro-Ribosome Inactivating Protein; proRIP; peptide linker; cancer;
 KW inactivation; eukaryotic ribosome; alpha fragment; beta fragment;
 KW inhibitor; protein synthesis; N-glycosidase; glycosidic bond; liver; rat;
 KW ribosomal 28S RNA; cellular proliferation; HIV-infected T cell.
 XX
 OS Bacteriophage H-19B.
 XX
 XX Key Location/Qualifiers
 FH 145..155
 FT Region /note= "Position of possible insertion of internal
 FT peptide linker sequence"
 FT
 FN US5635384-A.
 XX
 PD 03-JUN-1997.
 XX
 XX 26-JAN-1995; 95US-00378761.
 PF
 XX

PR 11-JUN-1990; 90US-00535636.
 PR 09-DEC-1992; 92US-00987927.
 XX PA (DOWC) DOWELANCO.
 XX PI Hey TD, Morgan AER, Walsh TA;
 XX DR WPI; 1997-309831/28.
 XX DR WPI; 1997-309831/28.
 XX PT Inactive precursor of maize ribosome-inactivating protein - also chimeric
 PT ribosome-inactivating protein precursors containing internal linker
 PT sequences.
 XX PS Claim 2; Col 113-116; 121pp; English.
 XX CC The sequences given in AAW21698-710 represent Ribosome Inactivating
 CC Proteins (RIP's), which may be used in the construction of the proRIP of
 CC the invention. The proRIP has a selectively removable, internal peptide
 CC linker. The precursor sequence is incapable of inactivating eukaryotic
 CC ribosomes, but can be converted by removal of the linker into a protein
 CC having alpha and beta fragments and being capable of inactivating
 CC eukaryotic ribosomes. RIPs are potent inhibitors of eukaryotic protein
 CC synthesis. They possess a highly specific N-glycosidase activity which
 CC cleaves the glycosidic bond of adenine 4324 of rat liver ribosomal 28S
 CC RNA. RIP's selectively inhibit cellular proliferation of cells, e.g. make
 CC cancer cells and HIV-infected T cells. The inactive proRIP proteins make
 CC it possible to provide protein synthesis inhibitors with uses in
 CC practical and improved ways not before possible. The RIP can be used to
 CC make cytotoxic conjugates. (Updated on 25-MAR-2003 to correct PF field.)
 CC (Updated on 17-OCT-2003 to standardise OS field)
 XX SQ Sequence 315 AA;
 Query Match 100.0%; Score 114; DB 2; Length 315;
 Best Local Similarity 100.0%; Pred. No. 1.1e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CHHHSRVARMASDEFFSMC 20
 DB 264 CHHHSRVARMASDEFFSMC 283
 RESULT 7
 AAW25139
 ID AAW25139 standard; protein; 315 AA.
 XX AC AAW25139;
 XX DT 25-MAR-2003 (revised)
 DT 02-DEC-1997 (first entry)
 DE SLT-1 (a ribosome inhibitory protein) inactive precursor.
 XX Maize; proRIP; ribosome inactivating protein; alpha; beta subunit;
 KW internal linker; Barley Translation Inhibitor; Trichosanthin;
 KW Ricin A-chain; Abrin-A A-chain; Saporin; SLT-1; Luffin A; MAP;
 KW Ricinus communis agglutinin; Momordin; PAP-S; Luffin-B; Dianthin 30;
 KW therapeutic toxin; tumour cell targeted; protein synthesis inhibitor;
 KW post-translational modification; cancer; neoplasia; HIV; AIDS;
 KW human immunodeficiency virus; acquired immune deficiency syndrome.
 XX OS Synthetic.
 XX US5646026-A.
 XX PD 08-JUL-1997.
 XX PF 07-JUN-1995; 95US-00485286.
 XX 11-JUN-1990; 90US-00535636.
 PR 09-DEC-1992; 92US-00987927.
 PR 26-JAN-1995; 95US-00378761.
 XX

PA (DOWC) DOWELANCO.
 XX Hey TD, Morgan AER, Walsh TA;
 XX DR WPI; 1997-362934/33.
 XX PT DNA encoding pro-ribosome inactivating proteins - inactive precursors of
 PT ribosome inactivating proteins; can be expressed in eukaryotic cells
 XX without causing cell death.
 XX PS Claim 4; Col 115-116; 186pp; English.
 XX CC AAW25139 represents an SLT-1 (a ribosome inhibitory protein, RIP) protein
 CC which was engineered to contain a selectively removable internal peptide
 CC linker sequence separating the alpha and beta units of the RIP. When
 CC separated the two units regain activity and are capable of inactivating
 CC eukaryotic ribosomes and hence preventing protein production. Many
 CC different RIPs may be produced with an internal linker including maize
 CC RIP, Trichosanthin, Ricin A-chain, Abrin-A A-chain and Saporin. The RIPs
 CC can be used in the construction of therapeutic toxins targeted to
 CC specific cells such as tumour cells via the attachment of a targeting
 CC polypeptide, e.g. a monoclonal antibody. A further use is in HIV therapy
 CC (see US4869903). There is interest in expressing RIP recombinantly in
 CC host eukaryotic cells, because of the capacity to provide correct post-
 CC translational processing. However, RIPs effectively inhibit protein
 CC synthesis in eukaryotic cells resulting in cell death. Since the inactive
 CC RIP proteins are not cytotoxic to eukaryotic cells, they can be
 CC recombinantly expressed in such cells and then converted to active RIP
 CC proteins. (Updated on 25-MAR-2003 to correct PF field.)
 XX SQ Sequence 315 AA;
 Query Match 100.0%; Score 114; DB 2; Length 315;
 Best Local Similarity 100.0%; Pred. No. 1.1e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CHHHSRVARMASDEFFSMC 20
 DB 264 CHHHSRVARMASDEFFSMC 283
 RESULT 8
 AAY96681
 ID AAY96681 standard; protein; 315 AA.
 XX AC AAY96681;
 XX DT 26-SEP-2000 (first entry)
 DE E. coli verotoxin 1 subunit A.
 XX VT-1; verotoxin; antitoxin therapy; fusion protein; affinity tag; food;
 KW recombinant production; screening; dairy; anti-bacterial; vaccine.
 OS Escherichia coli.
 XX US6080400-A.
 XX 27-JUN-2000.
 XX 13-MAR-1997; 97US-00816977.
 XX 24-MAR-1995; 95US-00410058.
 XX (OPHI-) OPHIDIAN PHARM INC.
 XX Williams JA, Byrne LM;
 XX WPI; 2000-451195/39.
 DR N-PSDB; AAAS1194.
 XX Bacterial cell for recombinantly expressing bacterial toxins in large
 PT quantities useful for immunization and treatment of bacterial infections,

PT comprises expression vector encoding bacterial toxin.
 PS Example 6; Col 69-71; 83pp; English.
 XX

CC The invention relates to antitoxin therapy for humans and other animals.
 CC Antitoxins which neutralize the pathologic effects of *Escherichia coli*
 CC toxins are generated by immunization of avian hosts with recombinant
 CC toxin fragments. The recombinant *E. coli* verotoxin (VT) is a fusion
 CC protein comprising a non-verotoxin protein (especially an affinity tag)
 CC fused to a portion of the VT-1 or VT-2 sequence. The VT B chains are
 CC small proteins (approximately 8 kDa), so use of a small affinity tag was
 CC preferred (i.e. polyhistidine). A polyhistidine affinity tag facilitates
 CC single step affinity purification of subunits from periplasmic extracts.
 CC However, due to poor recovery of his-tagged VT-1 A and VT-2 A chains,
 CC expression of maltose binding protein (MBP) fused subunits was
 CC undertaken. Due to the toxicity of the VT-2 B subunit, strict uninduced
 CC promoter control is necessary to permit cell viability. Bacterial host
 CC cells expressing a recombinant expression vector encoding a polyhistidine
 CC affinity tag and a portion of the VT-2 B chain are claimed. The vector is
 CC chosen from pET24hisVT2BL+, pET24hisVT2BL- and pET24VT2B, where "L+"
 CC indicates that the vector encodes the preprotein form of the protein and
 CC "L-" indicates that the vector encodes the mature form of the protein.
 CC The bacterial cell is capable of expressing large quantities (40 mg/l) of
 CC VT-2B. The toxins are useful for immunizing non-mammals and for detecting
 CC bacterial toxins in environmental samples including soil, water,
 CC industrial samples, biological samples and samples obtained from food and
 CC dairy processing instruments
 XX Sequence 315 AA;
 SQ

Query Match 100.0%; Score 114; DB 3; Length 315;
 Best Local Similarity 100.0%; Pred. No. 1.1e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHHSRVARVASDEFPSSMC 20
 |||||
 DB 264 CHHHSRVARVASDEFPSSMC 283

RESULT 9
 AAU77817
 ID AAU77817 standard; protein; 315 AA.
 AC
 XX AAU77817;
 XX
 DT 05-JUN-2002 (first entry)
 XX
 DE *E. coli* verotoxin VT1-A chain protein.
 XX
 KW Verotoxin; VT1-A; antitoxin; antidiarrheal; antibacterial; haemostatic;
 KW vaccine; haemorrhagic cystitis; balantitis; haemolytic uremic syndrome;
 KW thrombotic thrombocytopenic purpura.
 XX
 OS *Escherichia coli*.
 XX
 XX US2002012658-A1.
 PN
 XX 31-JAN-2002.
 PD
 XX 16-JUN-1999; 99US-00334477.
 PF
 XX 13-MAR-1997; 97US-00816977.
 PR
 XX (WILL/) WILLIAMS J A.
 PA (BYRN/) BYRNE L M.
 PA (PUGH/) PUGH C S G.
 XX
 PI Williams JA, Byrne LM, Pugh CSG;
 XX
 DR WPI; 2002-205094/26.
 DR N-PSDB; ABK11775.
 XX
 PT New recombinant expression vector encoding affinity tag and *Escherichia*

PT coli type 1 or type 2 verotoxin, useful for treating or preventing
 PT diseases due to *E. coli* verotoxins and in producing vaccines.
 XX Example 6; Page 38-39; 98pp; English.
 PS

CC This invention relates to a recombinant expression vector encoding an
 CC affinity tag and protein comprising at least a portion of a bacterial
 CC toxin consisting of *Escherichia coli* type 1 or type 2 verotoxin. The
 CC expression vector can be used to produce recombinant verotoxin protein
 CC which can be used to create a vaccine against diseases caused by *E. coli*
 CC such as verotoxin haemorrhagic cystitis and balantitis. The antitoxins
 CC are useful for treating humans and animals intoxicated with a bacterial
 CC toxin, particularly *E. coli* verotoxin. The antitoxins may also be used in
 CC the preventative treatment and in diagnostic assays to detect the
 CC presence of a toxin in a sample. The polypeptides derived from *E. coli*
 CC verotoxins are useful as immunogens for the production of vaccines,
 CC including multivalent vaccines and antitoxins, which can be administered
 CC to a subject at risk of diarrhoeal disease or at risk of developing extra
 CC -intestinal complications of *E. coli* infections, e.g. haemolytic uremic
 CC syndrome, thrombotic thrombocytopenic purpura. The present sequence
 CC represents the *E. coli* verotoxin protein VT1-A used to create the
 CC expression vectors of the invention
 XX Sequence 315 AA;
 SQ

Query Match 100.0%; Score 114; DB 5; Length 315;
 Best Local Similarity 100.0%; Pred. No. 1.1e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHHSRVARVASDEFPSSMC 20
 |||||
 DB 264 CHHHSRVARVASDEFPSSMC 283

RESULT 10
 ADC00545
 ID ADC00545 standard; protein; 315 AA.
 XX
 AC ADC00545;
 XX
 DT 04-DEC-2003 (first entry)
 XX
 DE Enterohaemorrhagic *E. coli* O157:H7-specific protein SEQ ID NO: 590.
 XX
 KW enterohaemorrhagic; anti-bacterial.
 XX
 OS *Escherichia coli*; O157:H7.
 XX
 PN JP2002355074-A.
 XX
 PD 10-DEC-2002.
 XX
 PF 24-JAN-2002; 2002JP-00015959.
 XX
 PR 24-JAN-2001; 2001JP-00112010.
 XX
 PA (UYTS-) UNIV TSUKUBA.
 XX
 XX WPI; 2003-451640/43.
 DR
 XX Enterohaemorrhagic *Escherichia coli* O157:H7-specific nucleic acid molecule
 XX and a polypeptide and its use, a polypeptide, a vector and a host cell.
 PT
 XX Claim 3; SEQ ID NO 590; 2067pp; Japanese.
 PS The invention relates to a novel enterohaemorrhagic *Escherichia coli*
 XX O157:H7-specific nucleic acid molecule. A polynucleotide of the invention
 CC has anti-bacterial activity. The polypeptide can be used in detection
 CC and/or treatment of O157:H7 infection. The nucleotide sequence of the
 CC genome of Enterohaemorrhagic *E. coli* O157:H7 was determined. The present
 CC sequence represents an *E. coli* O157:H7-specific polypeptide of the
 CC invention.
 XX


```

SQ Sequence 315 AA;
Query Match 100.0%; Score 114; DB 7; Length 315;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHHSRVARWASDEFFSMC 20
| | | | | | | | | | | | | | | | | | | | |
Db 264 CHHHSRVARWASDEFFSMC 283

RESULT 11
ADH34319
ID ADH34319 standard; protein; 315 AA.
XX
AC ADH34319;
XX
DT 11-MAR-2004 (first entry)
XX
DE Verotoxin 1 (VT1) A subunit.
XX
KW Attenuated verotoxin; attenuated VT; mutant A subunit; troponin I;
KW fusion protein; cancer; cytostatic; verotoxin 1; VT1; A subunit.
XX
OS Escherichia coli; O157:H7.
XX
FN WO2003066854-A1.
XX
PD 14-AUG-2003.
XX
PF 03-FEB-2003; 2003WO-JP001043.
XX
PR 04-FEB-2002; 2002JP-00026577.
XX
PA (YOSH/) YOSHIDA H.
XX
PI Yoshida H, Liu X;
XX
WPI; 2003-646309/61.
XX
Attenuated verotoxin controls tumor growth for treatment of cancer.
XX
Disclosure; Fig 3; 56pp; Japanese.
XX
The invention relates to attenuated verotoxins (VTs) comprising mutations
CC in one or more of the regions spanning residues 167-172 or 202-207 of the
CC mature verotoxin A subunit. The invention also relates to the mutant
CC verotoxin A subunit and the DNA encoding it; anticancer agents containing
CC the novel mutant A subunit; a fusion protein comprising the mutant
CC verotoxin A subunit and a ligand, especially troponin I, which binds to a
CC cancer cell; a fusion gene encoding the mutant A subunit/troponin I
CC fusion protein; and vectors encoding either the mutant verotoxin A
CC subunit, or the fusion gene of the invention. The attenuated verotoxins,
CC A subunits, fusion proteins, and polynucleotides encoding them are useful
CC in the treatment of cancer. The present sequence represents the A subunit
CC of verotoxin 1 (VT1).
XX
SQ Sequence 315 AA;
Query Match 100.0%; Score 114; DB 7; Length 315;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHHSRVARWASDEFFSMC 20
| | | | | | | | | | | | | | | | | | | | |
Db 264 CHHHSRVARWASDEFFSMC 283

RESULT 12
AAW25786
ID AAW25786 standard; protein; 316 AA.
XX
AC AAW25786;
XX

```

```

XX
DT 17-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 27-MAR-1998 (first entry)
XX
DE Phage H19B shiga-like toxin.
XX
KW Shiga-like toxin; slt-A gene; hybrid protein; cell delivery;
KW cell binding ligand; translocation domain; diphtheria toxin B';
KW interleukin-2; T-cell lymphoma; organ rejection; therapy; ss.
XX
OS Bacteriophage H-19B.
XX
FN US5668255-A.
XX
PD 16-SEP-1997.
XX
PF 04-AUG-1993; 93US-00102387.
XX
PR 07-JUN-1984; 84US-00618199.
PR 25-APR-1985; 85US-00726808.
PR 07-JUN-1985; 85US-00742554.
PR 22-DEC-1989; 89US-00456095.
PR 14-JUN-1990; 90US-00538276.
PR 27-JUN-1991; 91US-00722484.
XX
PA (SERA-) SERAGEN INC.
XX
PI Murphy JR;
XX
WPI; 1997-470103/43.
XX
N-PSDB; AAT91637.
XX
New hybrid molecules for delivery of agents to cells - comprise a binding
PT domain of a cell binding ligand and a portion of a trans-location domain
PT of a protein.
XX
Example 3; Fig 8A-C; 30pp; English.
XX
This protein comprises the Escherichia coli phage H19B Shiga-like toxin.
CC DNA (see AAT91637) encoding the A subunit of the Shiga-like toxin was
CC used to construct a Shiga-like toxin A-diphtheria toxin B'-interleukin-2
CC (SLTA-DTB'-IL2) gene that was expressed in E. coli. The hybrid protein
CC can be isolated and used to treat conditions involving over-production of
CC cells bearing IL2 receptors, such as certain i-cell lymphomas and organ
CC transplant rejection crises. The hybrid inactivates ribosomes in cells
CC bearing IL2 receptors, resulting in cessation of protein synthesis and
CC death of target cells. Claimed hybrid proteins comprise a translocation
CC domain and a cell binding domain from e.g. a hormone, growth factor or
CC protein toxin. The hybrid molecules can be used for the delivery of
CC agents (e.g. therapeutic genes, toxins, detectable labels) into cells.
CC The use of a translocation mechanism ensures that the hybrid will be
CC effective in relatively low doses, since a high proportion of the
CC subsequence of interest will be taken into the targeted cells. The hybrid
CC molecules can be manufactured as a single hybrid recombinant protein,
CC permitting reproducibility, consistency, and the precise control of
CC composition. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 17
CC -OCT-2003 to standardise OS field)
XX
SQ Sequence 316 AA;
Query Match 100.0%; Score 114; DB 2; Length 316;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHHSRVARWASDEFFSMC 20
| | | | | | | | | | | | | | | | | | | | |
Db 264 CHHHSRVARWASDEFFSMC 283

RESULT 13
AAW06407
ID AAW06407 standard; protein; 323 AA.

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```

XX AC AAW06407;
XX DT 25-FEB-1997 (first entry)
XX DE Histidine tagged verotoxinogenic E. coli toxin (VT1) subunit A.
XX KW Verotoxin; Escherichia coli; enteric infection; diarrhoea; vaccine;
XX KW haemolytic uraemic syndrome; detection.
XX OS Escherichia coli.
XX PN WO9630043-A1.
XX PD 03-OCT-1996.
XX PF 25-MAR-1996; 96WO-US004093.
XX PR 24-MAR-1995; 95US-00410058.
XX PA (OPHI-) OPHIDIAN PHARM INC.
XX PI Carroll SB, Stafford DC, Padhye NV;
XX WPI; 1996-505779/50.
XX DR N-PSDB; AAT42663.
XX Compens. contg. neutralising antitoxin against E.coli vero-toxin - used to
PT treat intoxicated individuals, and as a prophylactic against diarrhoeal
PT disease or extra-intestinal complications of E.coli infection.
XX Example 6; Page 61-62; 101pp; English.
XX Compositions containing neutralising antitoxin against one or more E.
CC coli verotoxin (VT) can be used to treat intoxicated adults and children
CC with enteric bacterial infections. They may also be used as prophylactics
CC e.g. as a vaccine, against diarrhoeal disease or the development of extra
CC -intestinal complications of E.coli infection, especially haemolytic
CC uraemic syndrome. The antitoxin can also be used to detect E. coli VT in
CC a sample. The VT is recombinant, preferably a fusion protein containing a
CC non-VT protein sequence and part of the E.coli VT1 or VT2 sequence. This
CC is a histidine tagged version of subunit A of VT1 as expressed from the
CC vector pET-23b
XX Sequence 323 AA;
    Query Match          100.0%; Score 114; DB 2; Length 323;
    Best Local Similarity 100.0%; Pred. No. 1.2e-10;
    Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHHSARVARMASDEFPSSMC 20
DB 264 CHHHSARVARMASDEFPSSMC 283

RESULT 14
AAV96686
ID AAV96686 standard; protein; 323 AA.
XX AAV96686;
XX 26-SEP-2000 (first entry)
XX Recombinant E. coli VT-1 A-polyhistidine fusion protein.
XX VT-1; verotoxin; antitoxin therapy; fusion protein; affinity tag; food;
XX recombinant production; screening; dairy; anti-bacterial; vaccine;
XX polyhistidine.
XX Escherichia coli.
XX Synthetic.
XX Chimeric.

```

```

FH Key Location/Qualifiers
FT Protein 1..315
FT /label= Verotoxin-1_subunit_A
FT Peptide 316..323
FT /label= Polyhistidine_affinity_tag
XX US6080400-A.
XX 27-JUN-2000.
XX 13-MAR-1997; 97US-00816977.
XX 24-MAR-1995; 95US-00410058.
XX (OPHI-) OPHIDIAN PHARM INC.
XX Williams JA, Byrne LM;
XX WPI; 2000-451195/39.
XX DR N-PSDB; AAS51208.
XX Bacterial cell for recombinantly expressing bacterial toxins in large
PT quantities useful for immunization and treatment of bacterial infections,
PT comprises expression vector encoding bacterial toxin.
XX Example 6; Col 89-90; 83pp; English.
XX The invention relates to antitoxin therapy for humans and other animals.
CC Antitoxins which neutralize the pathologic effects of Escherichia coli
CC toxins are generated by immunization of avian hosts with recombinant
CC toxin fragments. The recombinant E. coli verotoxin (VT) is a fusion
CC protein comprising a non-verotoxin protein (especially an affinity tag)
CC fused to a portion of the VT-1 or VT-2 sequence. The VT B chains are
CC small proteins (approximately 8 kDa), so use of a small affinity tag was
CC preferred (i.e. polyhistidine). A polyhistidine affinity tag facilitates
CC single step affinity purification of subunits from periplasmic extracts.
CC However, due to poor recovery of his-tagged VT-1 A and VT-2 A chains,
CC expression of maltose binding protein (MBP) fused subunits was
CC undertaken. Due to the toxicity of the VT-2 B subunit, strict uninduced
CC promoter control is necessary to permit cell viability. Bacterial host
CC cells expressing a recombinant expression vector encoding a polyhistidine
CC affinity tag and a portion of the VT-2 B chain are claimed. The vector is
CC chosen from pET24hisVT2BL+, pET24hisVT2BL- and pET24VT2B, where "L+"
CC "L-" indicates that the vector encodes the preprotein form of the protein and
CC "L-" indicates that the vector encodes the mature form of the protein.
CC The bacterial cell is capable of expressing large quantities (40 mg/l) of
CC VT-2B. The toxins are useful for immunizing non-mammals and for detecting
CC bacterial toxins in environmental samples including soil, water,
CC industrial samples, biological samples and samples obtained from food and
CC dairy processing instruments
XX Sequence 323 AA;
    Query Match          100.0%; Score 114; DB 3; Length 323;
    Best Local Similarity 100.0%; Pred. No. 1.2e-10;
    Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHHSARVARMASDEFPSSMC 20
DB 264 CHHHSARVARMASDEFPSSMC 283

RESULT 15
AAU77822
ID AAU77822 standard; protein; 323 AA.
XX AAU77822;
XX 05-JUN-2002 (first entry)
XX HIS-tagged E. coli VT-1A verotoxin protein.
XX Verotoxin; VT1-A; antitoxin; antidiarrheal; antibacterial; haemostatic;

```


KW vaccine; haemorrhagic cystitis; balantitis; haemolytic uremic syndrome;
 KW thrombotic thrombocytopenic purpura.

OS Escherichia coli.
 OS Synthetic.

FH Key Location/Qualifiers
 FT Peptide 316. .323
 FT /note= "C terminal peptide with HIS tag"

XX US2002012658-A1.

XX 31-JAN-2002.

XX PF 16-JUN-1999; 99US-00334477.

XX PR 13-MAR-1997; 97US-00816977.

XX PA (WILL/) WILLIAMS J A.

XX PA (BYRN/) BYRNE L M.

XX PA (PUGH/) PUGH C S G.

XX PI Williams JA, Byrne LM, Pugh CSG;

XX DR WPI; 2002-205094/26.

XX DR N-PSDB; ASK11789.

XX PT New recombinant expression vector encoding affinity tag and Escherichia
 PT coli type 1 or type 2 verotoxin, useful for treating or preventing
 PT diseases due to E. coli verotoxins and in producing vaccines.

XX PS Claim 1; Page 48-49; 98pp; English.

XX CC This invention relates to a recombinant expression vector encoding an
 CC affinity tag and protein comprising at least a portion of a bacterial
 CC toxin consisting of Escherichia coli type 1 or type 2 verotoxin. The
 CC expression vector can be used to produce recombinant verotoxin protein
 CC which can be used to create a vaccine against diseases caused by E. coli
 CC such as verotoxin haemorrhagic cystitis and balantitis. The antitoxins
 CC are useful for treating humans and animals intoxicated with a bacterial
 CC toxin, particularly E. coli verotoxin. The antitoxins may also be used in
 CC the preventative treatment and in diagnostic assays to detect the
 CC presence of a toxin in a sample. The polypeptides derived from E. coli
 CC verotoxins are useful as immunogens for the production of vaccines,
 CC including multivalent vaccines and antitoxins, which can be administered
 CC to a subject at risk of diarrhoeal disease or at risk of developing extra
 CC -intestinal complications of E. coli infections, e.g. haemolytic uremic
 CC syndrome, thrombotic thrombocytopenic purpura. The present sequence
 CC represents the HIS tagged E.coli VT1-A verotoxin protein of the invention

XX SQ Sequence 323 AA;

Query Match 100.0%; Score 114; DB 5; Length 323;
 Best Local Similarity 100.0%; Pred. No. 1.2e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHHSRVARMASDEFPSC 20

Db 264 CHHHSRVARMASDEFPSC 283

Search completed: February 10, 2006, 10:05:01
 Job time : 12.8856 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 10, 2006, 10:05:19 ; Search time 2.73063 Seconds
(without alignments)
704.723 Million cell updates/sec

Title: US-10-717-243-56

Perfect score: 114

Sequence: 1 CHHHSRVARMSDEFFPSMC 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_80.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	114	100.0	315	1	Shigella toxin cha
2	114	100.0	315	1	Shiga-like toxin c
3	114	100.0	315	2	Shiga-like toxin I
4	114	100.0	315	2	Shiga toxin I subu
5	114	100.0	315	2	Shiga toxin I subu
6	114	100.0	315	2	Shiga-like toxin I
7	50.5	44.3	365	2	hypothetical prote
8	50	43.9	451	2	hypothetical prote
9	49	43.0	2152	2	hypothetical prote
10	47	41.2	135	2	cell adhesion prot
11	47	41.2	252	2	conserved transcrip
12	46	40.4	196	2	probable transcrip
13	46	40.4	319	2	Shiga-like cytotox
14	46	40.4	507	2	pyridoxine 4-oxida
15	45	39.5	254	2	hypothetical prote
16	45	39.5	278	2	hypothetical prote
17	45	39.5	466	2	nicotinic acetylch
18	44	38.6	252	2	probable DNA-bindi
19	44	38.6	308	2	D-ribose-binding p
20	44	38.6	318	2	Shiga-like toxin I
21	44	38.6	319	2	variant shiga-like
22	44	38.6	319	2	shiga-like toxin I
23	44	38.6	319	2	Shiga-like toxin I
24	44	38.6	319	2	hypothetical prote
25	44	38.6	319	2	Shiga toxin 2 subu
26	44	38.6	319	2	Shiga toxin 2 subu
27	44	38.6	319	2	shiga-like toxin I
28	44	38.6	319	2	verocytotoxin A ch
29	44	38.6	320	2	shiga-like toxin -

30 44 38.6 433 2 T04594 aldehyde dehydroge
31 44 38.6 475 2 S45116 natriuretic peptid
32 44 38.6 535 2 A54155 natriuretic peptid
33 43 37.7 536 2 S71332 natriuretic peptid
34 43 37.7 540 1 OYHUCR natriuretic peptid
35 43 37.7 1149 2 T20891 hypothetical prote
36 43 37.7 2437 2 S53611 MIBP1 protein - ra
37 43 37.7 2500 1 WWHUE2 HIV-EP2 enhancer-b
38 42 36.8 161 2 S76282 hypothetical prote
39 42 36.8 285 2 B82842 spermidine synthas
40 42 36.8 381 2 S58663 isocitrate dehydro
41 42 36.8 387 2 T13147 isocitrate dehydro
42 42 36.8 398 2 AD2944 fosmidomycin resis
43 42 36.8 398 2 F98338 fosmidomycin resis
44 42 36.8 404 2 AB0376 probable membrane
45 42 36.8 406 1 JC5041 fosmidomycin resis

ALIGNMENTS

RESULT 1

A28626

Shigella toxin chain A precursor - Shigella dysenteriae

N;Alternate names: shiga toxin chain A

N;Contains: rRNA N-glycosidase (EC 3.2.2.22)

C;Species: Shigella dysenteriae

C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 09-Jul-2004

C;Accession: A28626; S04021

R;Strockbine, N.A.; Jackson, M.P.; Sung, L.M.; Holmes, R.K.; O'Brien, A.D.

J. Bacteriol. 170, 1116-1122, 1988

A;Title: Cloning and sequencing of the genes for Shiga toxin from Shigella dysenteriae

A;Reference number: A91864; MUID:88139166; PMID:2830229

A;Contents: Type 1 3818T

A;Accession: A28626

A;Molecule type: DNA

A;Residues: 1-315 <STR>

A;Cross-references: UNIPROT:Q8X696; UNIPARC:UPI00000000DA9; GB:M19437; NID:gl52784; PIDN:

R;Kozlov, Y.V.; Kabishev, A.A.; Fedchenko, V.I.; Baev, A.A.

Dokl. Biochem. 295, 216-220, 1987

A;Title: Cloning and primary structure of Shigella toxin genes.

A;Reference number: S04021

A;Accession: S04021

A;Molecule type: DNA

A;Residues: 1-315 <KOZ>

A;Cross-references: UNIPARC:UPI00000000DA9; EMBL:X07903; NID:G46946

C;Genetics:

A;Gene: stxA

C;Complex: heterohexamer of one A chain and five B chains (see PIR:XVEBBD)

C;Function:

A;Description: hydrolyzes the N-glycosidic bond of a specific adenine in 28S rRNA

C;Superfamily: Shigella toxin chain A

C;Keywords: cytotoxin; glycosidase; hexamer; hydrolase; RNA binding

F;1-22/Domain: signal sequence #status predicted <Sig>

F;23-315/Product: Shigella toxin chain A #status predicted <MAT>

Query Match 100.0%; Score 114; DB 1; Length 315;

Best Local Similarity 100.0%; Pred. No. 8e-11;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHSRVARMSDEFFPSMC 20

|||||

Db 264 CHHHSRVARMSDEFFPSMC 283

RESULT 2

XUBPH9

Shiga-like toxin chain A precursor - phage H19B

C;Species: phage H19B

A;Note: host Escherichia coli

C;Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 09-Jul-2004

C;Accession: A27052

R;Calderwood, S.B.; Auclair, F.; Donohue-Rolfe, A.; Keusch, G.T.; Mekalanos, J.J.


```

Proc. Natl. Acad. Sci. U.S.A. 84, 4364-4368, 1987
A;Title: Nucleotide sequence of the Shiga-like toxin genes of Escherichia coli.
A;Reference number: A27052; MUID:87260808; PMID:3299365
A;Accession: A27052
A;Molecule type: DNA
A;Residues: 1-315 <CAL>
A;Cross-references: UNIPROT:P08026; UNIPARC:UPI000000043F; GB:M16625; NID:g215043; PIDN:
C;Genetics:
A;Gene: sItA
C;Superfamily: Shigella toxin chain A
C;Keywords: toxin
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-315/Product: Shiga-like toxin chain A #status predicted <MAT>

Query Match 100.0%; Score 114; DB 1; Length 315;
Best Local Similarity 100.0%; Pred. No. 8e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHSRVARWASDEFFSMC 20
Db 264 CHHHSRVARWASDEFFSMC 283

RESULT 3
JN0725
Shiga-like toxin I chain A precursor [validated] - Escherichia coli
C;Species: Escherichia coli
C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
C;Accession: JN0732; I68043; I68043; A61473; S47254; S47256; S47258
R;Paton, A.W.; Paton, J.C.; Goldwater, P.N.; Heuzenroeder, M.W.; Manning, P.A.
Gene 129, 87-92, 1993
A;Title: Sequence of a variant Shiga-like toxin type-I operon of Escherichia coli O111:H
A;Reference number: JN0725; MUID:93328129; PMID:8335264
A;Accession: JN0725
A;Molecule type: DNA
A;Residues: 1-315 <PAT>
A;Cross-references: UNIPROT:Q47647; UNIPARC:UPI00000BC490; GB:L04539; NID:g147832; PIDN:
A;Experimental source: serotype O111:H(-)
R;Paton, A.W.; Beutin, L.; Paton, J.C.
Gene 153, 71-74, 1995
A;Title: Heterogeneity of the amino-acid sequences of Escherichia coli Shiga-like toxin
A;Reference number: I53932; MUID:95189106; PMID:7883188
A;Accession: I53932
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-170,'S',172-248,'E',250-315 <PAT1>
A;Cross-references: UNIPARC:UPI00000BA3CB; EMBL:Z36899; NID:g534987; PIDN:CAA85366.1; PI
A;Experimental source: serotype O48:H21
A;Note: submitted to the EMBL Data Library, August 1994
A;Accession: I68041
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-131,'S',133-170,'S',172-315 <PAT2>
A;Cross-references: UNIPARC:UPI00000B9ECB; EMBL:Z36900; NID:g535054; PIDN:CAA85368.1; PI
A;Experimental source: serotype O111:H(-)
A;Note: submitted to the EMBL Data Library, August 1994
A;Accession: I68043
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-170,'S',172-250,'V',252-273,'IVPN',278-284,'V',286-308,'I',310-311,'A',313
A;Cross-references: UNIPARC:UPI000005D32; EMBL:Z36901; NID:g535088; PIDN:CAA85370.1; PI
R;Takao, T.; Tanabe, T.; Hong, Y.M.; Shimonishi, Y.; Kurazono, H.; Yutsudo, T.; Sasakawa
Microb. Pathog. 5, 357-369, 1988
A;Title: Identity of molecular structure of Shiga-like toxin I (VT1) from Escherichia co
A;Reference number: A61473
A;Accession: C61473
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-170,'S',172-315 <PAT1>
A;Cross-references: UNIPARC:UPI0000000DA9
A;Experimental source: strain O157:H7
A;Accession: A61473

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```

A;Status: preliminary
A;Molecule type: protein
A;Residues: 23-51;762-76107-132,'XX',135-136;183-192;202-224,'XX',227-241;276-282,291-29
A;Cross-references: UNIPARC:UPI00001766F7; UNIPARC:UPI00001766F8; UNIPARC:UPI00001766F9;
A;Experimental source: strain O157:H7
C;Genetics:
A;Gene: SLT-1A
C;Superfamily: Shigella toxin chain A
C;Keywords: disulfide bond; toxin
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-315/Product: Shiga-like toxin I chain A #status experimental <MAT>

Query Match 100.0%; Score 114; DB 2; Length 315;
Best Local Similarity 100.0%; Pred. No. 8e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHSRVARWASDEFFSMC 20
Db 264 CHHHSRVARWASDEFFSMC 283

RESULT 4
F91000
Shiga toxin I subunit A precursor [imported] - Escherichia coli (strain O157:H7, substra
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: F91000
R;Hayashi, T.; Makino, K.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: F91000
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-315 <HAY>
A;Cross-references: UNIPROT:Q8X696; UNIPARC:UPI0000000DA9; GB:BA0000007; PIDN:BA836397.1;
A;Experimental source: strain O157:H7, substrain RMD 0509952
C;Genetics:
A;Gene: ECa2974
C;Superfamily: Shigella toxin chain A

Query Match 100.0%; Score 114; DB 2; Length 315;
Best Local Similarity 100.0%; Pred. No. 8e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHSRVARWASDEFFSMC 20
Db 264 CHHHSRVARWASDEFFSMC 283

RESULT 5
H85845
Shiga toxin I subunit A precursor [imported] - Escherichia coli (strain O157:H7, substra
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: H85845
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: H85845
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-315 <STO>
A;Cross-references: UNIPROT:Q8X696; UNIPARC:UPI0000000DA9; GB:AE005174; NID:g12516395; P
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: stx1A
C;Superfamily: Shigella toxin chain A

Query Match 100.0%; Score 114; DB 2; Length 315;

```


A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-451 <ANT>
A;Cross-references: UNIPROT:C9TYW1; UNIPARC:UPI000007570D; EMBL:AF100675; PIDN:AAC69004.
A;Experimental source: strain Bristol N2; clone Y5SH10A
C;Genetics:
A;Gene: CESP:Y5SH10A.1
A;Map position: 4
A;Introns: 29/2; 57/1; 95/3; 233/1; 319/3
C;Superfamily: Caenorhabditis elegans hypothetical protein Y5SH10A.1

Query Match 43.9%; Score 50; DB 2; Length 451;
Best Local Similarity 58.8%; Pred. No. 2.8;
Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 HHASRVARMASDRFPS 18
| : ||| : ||| |
Db 151 HEKSRVKRATDEFNS 167

RESULT 9
T45583
hypothetical protein F11C1.210 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C;Accession: T45583
R;Bargues, M.; Collado, M.C.; Navarro, P.; Terol, J.; Perez-Alonso, M.; Mewes, H.W.; May submitted to the Protein Sequence Database, December 1999
A;Reference number: 223007
A;Accession: T45583
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-2152 <BAR>
A;Cross-references: UNIPROT:Q9SND1; UNIPARC:UPI000009D156; EMBL:ALJ32976
A;Experimental source: cultivar Columbia; BAC clone F11C1
C;Genetics:
A;Map position: 3
A;Introns: 53/3; 411/2; 1479/3; 1543/2; 1592/3; 1659/1; 1750/1; 1965/3
A;Note: F11C1.210

Query Match 43.0%; Score 49; DB 2; Length 2152;
Best Local Similarity 41.2%; Pred. No. 20;
Matches 7; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 3 HHASRVARMASDRFPS 19
| : ||| : ||| |
Db 131 HHVKVATLRGEDFPPL 147

RESULT 10
A34653
cell adhesion protein SQM1 - human
C;Species: Homo sapiens (man)
C;Date: 06-Jul-1990 #sequence_revision 06-Jul-1990 #text_change 09-Jul-2004
C;Accession: A34653
R;Wong, Y.C.; Tsao, S.W.; Kakefuda, M.; Bernal, S.D.
Biochem. Biophys. Res. Commun. 166, 984-992, 1990
A;Title: cDNA cloning of a novel cell adhesion protein expressed in human squamous carcinoma cell lines
A;Reference number: A34653; MUID:90147818; PMID:2302251
A;Accession: A34653
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-135 <WON>
A;Cross-references: UNIPROT:P17568; UNIPARC:UPI000014AAD6; GB:M33374; NID:g180232; PIDN:
C;Keywords: cell adhesion

Query Match 41.2%; Score 47; DB 2; Length 135;
Best Local Similarity 44.4%; Pred. No. 2.5;
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 CHHHSRVARMASDRFPS 18
| : ||| : ||| |
Db 58 CAHHILRLCKRDSFPS 75

RESULT 11
D95853
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C;Accession: D95853
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endo
A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: D95853
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-252 <KUR>
A;Cross-references: UNIPROT:Q92X70; UNIPARC:UPI00000C33EA; GB:AL591985; PIDN:CAC48492.1;
A;Experimental source: strain 1021, megaplasmid pSymB
R;Galibert F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
A;Contents: annotation
C;Genetics:
A;Gene: Smb20092
A;Genome: plasmid

Query Match 41.2%; Score 47; DB 2; Length 252;
Best Local Similarity 52.9%; Pred. No. 4.7;
Matches 9; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CHHHSRVARVASDEFP 17
Db 224 CRVHGSLRASDHLP 240

RESULT 12
D83279
Probable transcription regulator PA2931 [imported] - Pseudomonas aeruginosa (strain PA01
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: D83279
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: D83279
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-196 <STO>
A;Cross-references: UNIPROT:Q9H2R6; UNIPARC:UPI00000C588E; GB:AE004719; GB:AE004091; NID
C;Genetics:
A;Experimental source: strain PA01
A;Gene: PA2931

Query Match 40.4%; Score 46; DB 2; Length 196;
Best Local Similarity 69.2%; Pred. No. 5.3;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 8 VARMSDEFPSC 20
Db 95 VARFCSDEFPRC 107

RESULT 13
I60446
Shiga-like cytotoxin subunit A - Escherichia coli

N;Alternate names: shiga-like toxin II variant chain A
C;Species: Escherichia coli
C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
C;Accession: I60446; MUID:157048; S31420
R;Paton, A.W.; Paton, J.C.; Heuzenroeder, M.W.; Goldwater, P.N.; Manning, P.A.
Microb. Pathog. 13, 225-236, 1992
A;Title: Cloning and nucleotide sequence of a variant Shiga-like toxin II gene from Eschi
A;Reference number: I60446; MUID:93180660; PMID:1291844
A;Accession: I60446
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-319 <RES>
A;Cross-references: UNIPROT:Q03037; UNIPARC:UPI00000BEE9B; EMBL:X65949; NID:949089; PIDN:
R;Paton, A.W.; Paton, J.C.; Manning, P.A.
Microb. Pathog. 15, 77-82, 1993
A;Title: Polymerase chain reaction amplification, cloning and sequencing of variant Esch
A;Reference number: I57048; MUID:94018566; PMID:8412629
A;Accession: I57048
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-197; G, 199-319 <RE2>
A;Cross-references: UNIPARC:UPI000016F4EF; GB:L11078; NID:G304950; PIDN:AAA16360.1; PID:
C;Superfamily: Shigella toxin chain A
C;Keywords: cytotoxin

Query Match 40.4%; Score 46; DB 2; Length 319;
Best Local Similarity 35.0%; Pred. No. 8.7;
Matches 7; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

Qy 1 CHHHSRVARVASDEFPSC 20
Db 263 CHHQSRSRVAVNEIQPEC 282

RESULT 14
JC7855
Pyridoxine 4-oxidase (EC 1.1.3.12) - Microbacterium luteolum YK-1
N;Alternate names: PN 4-oxidase; pyridoxin 4-oxidase
C;Species: Microbacterium luteolum YK-1
C;Date: 18-Nov-2002 #sequence_revision 18-Nov-2002 #text_change 05-Oct-2004
C;Accession: JC7855; PC7192
R;Kaneda, Y.; Ohnishi, K.; Yagi, T.
Biosci. Biotechnol. Biochem. 66, 1022-1031, 2002
A;Title: Purification, Molecular cloning, and characterization of pyridoxine 4-oxidase f
A;Reference number: JC7855; MUID:22087109; PMID:12092811
A;Accession: JC7855
A;Molecule type: DNA
A;Residues: 1-507 <KAN>
A;Cross-references: UNIPARC:UPI000017CE48; DDBJ:AB049341
A;Experimental source: strain YK-1
A;Accession: PC7192
A;Molecule type: protein
A;Residues: 2-20;348-364 <KA2>
A;Cross-references: UNIPARC:UPI000017CE49; UNIPARC:UPI000017CE4A
C;Comment: This enzyme that is an FAD-dependent enzyme and a monomeric protein belongs t
ors to form pyridoxal and hydrogen peroxide or reduced forms of the acceptors. This enzy
C;Genetics:
A;Gene: pno
C;Superfamily: alcohol oxidase
C;Keywords: oxidoreductase

Query Match 40.4%; Score 46; DB 2; Length 507;
Best Local Similarity 57.1%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 HHHSRVARVASDE 15
Db 446 HHHSRVARVASDE 459

RESULT 15
S72759
hypothetical protein B1496_C2_188 - Mycobacterium leprae

C;Species: Mycobacterium leprae
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S72759; T11014
R;Smith, D.R.; Robison, K.
submitted to the EMBL Data Library, November 1993
A;Description: Mycobacterium leprae cosmid B1496.
A;Reference number: S72695
A;Accession: S72759
A;Molecule type: DNA
A;Residues: 1-254 <SMI>
A;Cross-references: UNIPROT:Q49688; UNIPARC:UPI00000D433C; EMBL:U00013; NID:g466868; PID
R;Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, September 1997
A;Reference number: Z16918
A;Accession: T11014
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-254 <PAR>
A;Cross-references: UNIPARC:UPI00000D433C; EMBL:Z99125; NID:g2398683; PIDN:CAB16173.1; E
C;Genetics:
A;Gene: MLC1536.29c
A;Start codon: GTG

Query Match 39.5%; Score 45; DB 2; Length 254;
Best Local Similarity 45.5%; Pred. No. 10;
Matches 10; Conservative 2; Mismatches 4; Indels 6; Gaps 2;

QY. 1 CHHH--ASRVARMASDEFFSMC 20
||| ||| :||| :
Db 196 QHHCPSVSHA----EEFPELC 213

Search completed: February 10, 2006, 10:14:04
Job time : 3.73063 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 10, 2006, 10:00:34 ; Search time 16.9004 Seconds
(without alignments)
834.927 Million cell updates/sec

Title: US-10-717-243-56

Perfect score: 114

Sequence: 1 CHHHSRVARMASDEFFPSMC 20

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	114	100.0	222	Q5ZPW9_ECOLI	Q5zpw9 escherichia
2	114	100.0	236	Q5ZPX0_ECOLI	Q5zpx0 escherichia
3	114	100.0	237	Q5ZPX1_ECOLI	Q5zpx1 escherichia
4	114	100.0	240	Q5ZPX2_ECOLI	Q5zpx2 escherichia
5	114	100.0	242	Q5ZPX4_ECOLI	Q5zpx4 escherichia
6	114	100.0	243	Q5ZPX3_ECOLI	Q5zpx3 escherichia
7	114	100.0	243	Q5ZPX5_ECOLI	Q5zpx5 escherichia
8	114	100.0	248	Q5ZPX6_ECOLI	Q5zpx6 escherichia
9	114	100.0	254	Q5ZPX8_ECOLI	Q5zpx8 escherichia
10	114	100.0	259	Q5ZPX9_ECOLI	Q5zpx9 escherichia
11	114	100.0	276	Q5ZPY0_ECOLI	Q5zpy0 escherichia
12	114	100.0	313	Q5ZPY1_ECOLI	Q5zpy1 escherichia
13	114	100.0	315	Q5ZPY2_ECOLI	Q5zpy2 escherichia
14	114	100.0	315	Q5ZPY3_ECOLI	Q5zpy3 escherichia
15	114	100.0	315	Q5ZPY4_ECOLI	Q5zpy4 escherichia
16	114	100.0	315	Q5ZPY5_ECOLI	Q5zpy5 escherichia
17	114	100.0	315	Q5ZPY6_ECOLI	Q5zpy6 escherichia
18	114	100.0	315	Q5ZPY7_ECOLI	Q5zpy7 escherichia
19	114	100.0	315	Q5ZPY8_ECOLI	Q5zpy8 escherichia
20	114	100.0	315	Q5ZPY9_ECOLI	Q5zpy9 escherichia
21	114	100.0	315	Q5ZPY10_ECOLI	Q5zpy10 escherichia
22	114	100.0	315	Q5ZPY11_ECOLI	Q5zpy11 escherichia
23	114	100.0	315	Q5ZPY12_ECOLI	Q5zpy12 escherichia
24	114	100.0	315	Q5ZPY13_ECOLI	Q5zpy13 escherichia
25	114	100.0	315	Q5ZPY14_ECOLI	Q5zpy14 escherichia
26	114	100.0	315	Q5ZPY15_ECOLI	Q5zpy15 escherichia
27	114	100.0	315	Q5ZPY16_ECOLI	Q5zpy16 escherichia
28	114	100.0	315	Q5ZPY17_ECOLI	Q5zpy17 escherichia
29	114	100.0	315	Q5ZPY18_ECOLI	Q5zpy18 escherichia
30	114	100.0	315	Q5ZPY19_ECOLI	Q5zpy19 escherichia
31	114	100.0	315	Q5ZPY20_ECOLI	Q5zpy20 escherichia

32 114 100.0 315 2 Q77M7_9CAUD Q77m7 phage phi 4
33 105 92.1 315 2 Q83XK3_ECOLI Q83xk3 escherichia
34 96 84.2 315 2 Q94M00_9VIRU Q94m00 bacterioph
35 96 84.2 315 2 Q47640_ECOLI Q47640 escherichia
36 96 84.2 315 2 Q8V67_9VIRU Q8v67 escherichia
37 90 78.9 315 2 Q8V64_9VIRU Q8v64 escherichia
38 89 78.1 251 2 Q5ZPX7_ECOLI Q5zpx7 escherichia
39 86 75.4 315 2 Q8L168_ECOLI Q8l168 escherichia
40 52 45.6 427 2 Q4UWU4_XANCP Q4uwu4 xanthomonas
41 52 45.6 427 2 Q8P7A8_XANCP Q8p7a8 xanthomonas
42 50.5 44.3 365 2 Q9T035_9VIRU Q9t035 arabisdopsis
43 50 43.9 373 2 Q4T41_9VIRU Q4t41 tetraodon n
44 50 43.9 451 2 Q9TYW1_CAREL Q9tyw1 caenorhabdi
45 49 43.0 325 2 Q56W68_9VIRU Q56w68 arabisdopsis

ALIGNMENTS

RESULT 1
ID Q5ZPW9_ECOLI PRELIMINARY; PRT; 222 AA.
AC Q5ZPW9;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Verocytotoxin 1 (Fragment).
GN Name=VT1;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC CATRAINE-372;
RA Catarame T.M.;
RT "Rapid Diagnostic Methods for Food Borne Pathogens.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ537526; CAD68999.1; -; Genomic_DNA.
DR SMR; Q5ZPW9: 1-222.
DR GO; GO:0016787; P:hydrolase activity; IEA.
DR GO; GO:0030598; P:RNA N-glycosylase activity; IEA.
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
FT NON TER 1 1
FT NON TER 222 222
SQ SEQUENCE 222 AA; 24698 MW; F29BF3CE24419E29 CRC64;

Query Match 100.0%; Score 114; DB 2; Length 222;
Best Local Similarity 100.0%; Pred. No. 4.2e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHSRVARMASDEFFPSMC 20
|||||
Db 196 CHHHSRVARMASDEFFPSMC 215

RESULT 2
ID Q5ZPX0_ECOLI PRELIMINARY; PRT; 236 AA.
AC Q5ZPX0;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Verocytotoxin 1 (Fragment).
GN Name=VT1;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.


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OX NCBI_TaxID=562;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=348;
RA Catarama T.M.;
RT "Rapid Diagnostic Methods for Food Borne Pathogens.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ537525; CAD68998.1; -, Genomic_DNA.
DR SMR; Q52PX0; 1-236.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
FT NON_TER 1
FT NON_TER 236
SQ SEQUENCE 236 AA; 26045 MW; F8EEDF81890F04C0 CRC64;

Query Match 100.0%; Score 114; DB 2; Length 236;
Best Local Similarity 100.0%; Pred. No. 4.5e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHSRVARVASDEFPFPMC 20
Db 207 CHHHSRVARVASDEFPFPMC 226

RESULT 3
Q52PX1 ECOLI
ID Q52PX1 ECOLI PRELIMINARY; PRT; 237 AA.
AC Q52PX1;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Verocytotoxin 1 (Fragment).
GN Name=Vtl;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=333;
RA Catarama T.M.;
RT "Rapid Diagnostic Methods for Food Borne Pathogens.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ537524; CAD68997.1; -, Genomic_DNA.
DR SMR; Q52PX1; 1-237.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
FT NON_TER 1
FT NON_TER 237
SQ SEQUENCE 237 AA; 26182 MW; D578EEDF81890F04 CRC64;

Query Match 100.0%; Score 114; DB 2; Length 237;
Best Local Similarity 100.0%; Pred. No. 4.5e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHSRVARVASDEFPFPMC 20
Db 207 CHHHSRVARVASDEFPFPMC 226

RESULT 4
Q52PX2 ECOLI
ID Q52PX2 ECOLI PRELIMINARY; PRT; 240 AA.
AC Q52PX2;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Verocytotoxin 1 (Fragment).
GN Name=Vtl;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=359;
RA Catarama T.M.;
RT "Rapid Diagnostic Methods for Food Borne Pathogens.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ537523; CAD68996.1; -, Genomic_DNA.
DR SMR; Q52PX2; 1-240.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
FT NON_TER 1
FT NON_TER 240
SQ SEQUENCE 240 AA; 26538 MW; B46AA23578EEDF81 CRC64;

Query Match 100.0%; Score 114; DB 2; Length 240;
Best Local Similarity 100.0%; Pred. No. 4.6e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHSRVARVASDEFPFPMC 20
Db 207 CHHHSRVARVASDEFPFPMC 226

RESULT 5
Q52PX4 ECOLI
ID Q52PX4 ECOLI PRELIMINARY; PRT; 242 AA.
AC Q52PX4;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Verocytotoxin 1 (Fragment).
GN Name=Vtl;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=354;
RA Catarama T.M.;
RT "Rapid Diagnostic Methods for Food Borne Pathogens.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ537521; CAD68994.1; -, Genomic_DNA.
DR SMR; Q52PX4; 1-242.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
FT NON_TER 1
FT NON_TER 242
SQ SEQUENCE 242 AA; 26615 MW; A32A72928BB03D43 CRC64;
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Query Match 100.0%; Score 114; DB 2; Length 242;
 Best Local Similarity 100.0%; Pred. No. 4.6e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CHHHSRVARWASDEFPSSMC 20
 |||||
 Db 216 CHHHSRVARWASDEFPSSMC 235

RESULT 6

Q5ZPX3_ECOLI
 ID Q5ZPX3_ECOLI PRELIMINARY; PRT; 243 AA.
 AC Q5ZPX3;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Verocytotoxin 1 (Fragment).
 GN Name=Vtl;
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=352;
 RA Catarame T.M.;
 RT "Rapid Diagnostic Methods for Food Borne Pathogens.";
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ537522; CAD68995.1; -, Genomic_DNA.
 DR SMR; Q5ZPX3; 1-243.

DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR GO; GO:0030598; F:RNA N-glycosylase activity; IEA.
 DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 FT NON_TER 1
 FT NON_TER 243
 SQ SEQUENCE 243 AA; 26765 MW; 1858F46958FD9469 CRC64;

Query Match 100.0%; Score 114; DB 2; Length 243;
 Best Local Similarity 100.0%; Pred. No. 4.6e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CHHHSRVARWASDEFPSSMC 20
 |||||
 Db 209 CHHHSRVARWASDEFPSSMC 228

RESULT 7

Q5ZPX5_ECOLI
 ID Q5ZPX5_ECOLI PRELIMINARY; PRT; 243 AA.
 AC Q5ZPX5;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Verocytotoxin 1 (Fragment).
 GN Name=Vtl;
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=381;
 RA Catarame T.M.;
 RT "Rapid Diagnostic Methods for Food Borne Pathogens.";
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ537520; CAD68993.1; -, Genomic_DNA.
 DR SMR; Q5ZPX5; 1-243.

DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR GO; GO:0030598; F:RNA N-glycosylase activity; IEA.
 DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 FT NON_TER 1
 FT NON_TER 243
 SQ SEQUENCE 243 AA; 26617 MW; 4A69B4A3538DE250 CRC64;

Query Match 100.0%; Score 114; DB 2; Length 243;
 Best Local Similarity 100.0%; Pred. No. 4.6e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CHHHSRVARWASDEFPSSMC 20
 |||||
 Db 218 CHHHSRVARWASDEFPSSMC 237

RESULT 8

Q5ZPX6_ECOLI
 ID Q5ZPX6_ECOLI PRELIMINARY; PRT; 248 AA.
 AC Q5ZPX6;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Verocytotoxin 1 (Fragment).
 GN Name=Vtl;
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=CHI;
 RA Catarame T.M.;
 RT "Rapid Diagnostic Methods for Food Borne Pathogens.";
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ537519; CAD68992.1; -, Genomic_DNA.
 DR SMR; Q5ZPX6; 4-248.

DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR GO; GO:0030598; F:RNA N-glycosylase activity; IEA.
 DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 FT NON_TER 1
 FT NON_TER 248
 SQ SEQUENCE 248 AA; 27189 MW; 653792826D462PED CRC64;

Query Match 100.0%; Score 114; DB 2; Length 248;
 Best Local Similarity 100.0%; Pred. No. 4.7e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CHHHSRVARWASDEFPSSMC 20
 |||||
 Db 222 CHHHSRVARWASDEFPSSMC 241

RESULT 9

Q5ZPX8_ECOLI
 ID Q5ZPX8_ECOLI PRELIMINARY; PRT; 254 AA.
 AC Q5ZPX8;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Verocytotoxin 1 (Fragment).
 GN Name=Vtl;
 OS Escherichia coli.


```
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=361;
RA Catarame T.M.;
RT "Rapid Diagnostic Methods for Food Borne Pathogens.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ537517; CAD68990.1; -; Genomic_DNA.
DR SMR; Q52PX8; 1-254.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
FT NON_TER 1 254
FT NON_TER 254 254
SQ SEQUENCE 254 AA; 27842 MW; AC3BF7F69D9D1A52 CRC64;

Query Match 100.0%; Score 114; DB 2; Length 254;
Best Local Similarity 100.0%; Pred. No. 4.8e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHSRVARMSDEFFPSMC 20
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Db 228 CHHHSRVARMSDEFFPSMC 247

RESULT 10
Q52PX9_ECOLI PRELIMINARY; PRT; 259 AA.
AC Q52PX9;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Verocytotoxin 1 (Fragment).
GN Name=Vtl;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=332;
RA Catarame T.M.;
RT "Rapid Diagnostic Methods for Food Borne Pathogens.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ537516; CAD68989.1; -; Genomic_DNA.
DR SMR; Q52PX9; 15-259.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
FT NON_TER 1 259
FT NON_TER 259 259
SQ SEQUENCE 259 AA; 28482 MW; 774B2B9CD18F9175 CRC64;

Query Match 100.0%; Score 114; DB 2; Length 259;
Best Local Similarity 100.0%; Pred. No. 5e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHSRVARMSDEFFPSMC 20
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Db 233 CHHHSRVARMSDEFFPSMC 252

RESULT 11
Q52PY0_ECOLI PRELIMINARY; PRT; 276 AA.
AC Q52PY0;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Verocytotoxin 1 (Fragment).
GN Name=Vtl;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=378;
RA Catarame T.M.;
RT "Rapid Diagnostic Methods for food Borne Pathogens.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ537515; CAD68988.1; -; Genomic_DNA.
DR SMR; Q52PY0; 1-276.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
FT NON_TER 1 276
FT NON_TER 276 276
SQ SEQUENCE 276 AA; 30213 MW; 2BE68939E84D6378 CRC64;

Query Match 100.0%; Score 114; DB 2; Length 276;
Best Local Similarity 100.0%; Pred. No. 5.3e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHSRVARMSDEFFPSMC 20
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Db 233 CHHHSRVARMSDEFFPSMC 252

RESULT 12
Q7WZ18_ECO57 PRELIMINARY; PRT; 313 AA.
AC Q7WZ18;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Shiga toxin 1 variant A subunit.
GN Name=stx1;
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AI2000/182;
RA Suzuki M.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB083043; BAC78637.1; -; Genomic_DNA.
DR HSSP; Q9FBI2; 1DM0.
DR SMR; Q7WZ18; 23-312.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
SQ SEQUENCE 313 AA; 34639 MW; DDF7ABF58F30BD19 CRC64;

Query Match 100.0%; Score 114; DB 2; Length 313;
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHSRVARMASDEFFSMC 20
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Db 264 CHHHSRVARMASDEFFSMC 283

RESULT 15

Q5MBW7_9CAUD
ID Q5MBW7_9CAUD PRELIMINARY; PRT; 315 AA.
AC Q5MBW7;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE StxAl.
GN Name=stxAl;
OS Stx1-converting phage phi-O153.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
OC Lambda-like viruses.
OX NCBI_TaxID=305853;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Karalius B.J., Butterton J.R.;
RT "Nucleotide sequence of stx region of Stx1-producing rabbit E. coli strain 0153:H-";
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY838795; AAW21758.1; -; Genomic_DNA.
DR SMR; Q5MBW7; 23-312.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PROSITE; PS00275; SHIGA RICIN; 1.
KW Hydrolase; Protein synthesis inhibitor; Toxin.
SQ SEQUENCE 315 AA; 34813 MW; 8A423DP7ABF58F30 CRC64;

Query Match 100.0%; Score 114; DB 2; Length 315;

Best Local Similarity 100.0%; Pred. No. 6.1e-10;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHSRVARMASDEFFSMC 20
| | | | | | | | | | | | | | | |
Db 264 CHHHSRVARMASDEFFSMC 283

Search completed: February 10, 2006, 10:12:46

Job time : 18.9004 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 10, 2006, 10:13:09 ; Search time 3.98524 Seconds
(without alignments)
414.909 Million cell updates/sec

Title: US-10-717-243-56

Perfect score: 114

Sequence: 1 CHHARSVARWASDEFFSMC 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA.*

- 1: /cgm2_6/ptodata/1/iaa/5 COMB.pep.*
- 2: /cgm2_6/ptodata/1/iaa/6 COMB.pep.*
- 3: /cgm2_6/ptodata/1/iaa/H COMB.pep.*
- 4: /cgm2_6/ptodata/1/iaa/PCUS COMB.pep.*
- 5: /cgm2_6/ptodata/1/iaa/RE COMB.pep.*
- 6: /cgm2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	114	100.0	20	1	US-07-988-430-58
2	114	100.0	20	1	US-08-425-336-56
3	114	100.0	20	1	US-08-488-113B-56
4	114	100.0	20	1	US-08-477-484B-56
5	114	100.0	20	1	US-08-646-360-56
6	114	100.0	20	2	US-08-839-765-56
7	114	100.0	20	2	US-09-136-389-56
8	114	100.0	20	2	US-09-610-838-56
9	114	100.0	20	2	US-09-711-485-56
10	114	100.0	20	4	PCT-US92-09487-58
11	114	100.0	315	1	US-08-378-761A-73
12	114	100.0	315	1	US-08-485-286-73
13	114	100.0	315	2	US-08-816-977-2
14	114	100.0	315	2	US-09-334-477-2
15	114	100.0	323	2	US-08-816-977-21
16	114	100.0	323	2	US-09-334-477-21
17	114	100.0	326	2	US-08-816-977-37
18	114	100.0	326	2	US-09-334-477-37
19	114	100.0	332	1	US-08-621-803-251
20	114	100.0	332	2	US-09-217-352-251
21	114	100.0	690	2	US-08-816-977-47
22	114	100.0	690	2	US-09-334-477-47
23	114	100.0	708	2	US-08-816-977-33
24	114	100.0	708	2	US-09-334-477-33
25	47	41.2	135	1	US-08-757-036-3
26	46	40.4	204	2	US-09-252-991A-18665
27	45	39.5	413	2	US-09-328-352-5860

28	45	39.5	525	2	US-09-252-991A-28266	Sequence 28266, A
29	44	38.6	138	1	US-08-757-036-1	Sequence 1, Appli
30	44	38.6	297	1	US-08-180-761B-2	Sequence 2, Appli
31	44	38.6	318	2	US-08-816-977-6	Sequence 6, Appli
32	44	38.6	318	2	US-09-334-477-6	Sequence 6, Appli
33	44	38.6	319	1	US-08-180-761B-1	Sequence 1, Appli
34	44	38.6	326	2	US-08-816-977-25	Sequence 25, Appli
35	44	38.6	326	2	US-09-334-477-25	Sequence 25, Appli
36	44	38.6	329	2	US-08-816-977-39	Sequence 39, Appli
37	44	38.6	329	2	US-09-334-477-39	Sequence 39, Appli
38	44	38.6	360	2	US-09-252-991A-28104	Sequence 28104, A
39	44	38.6	433	2	US-09-344-882-26	Sequence 26, Appli
40	44	38.6	433	2	US-10-293-865-26	Sequence 26, Appli
41	44	38.6	450	2	US-09-252-991A-24440	Sequence 24440, A
42	44	38.6	575	2	US-09-107-532A-3910	Sequence 3910, Ap
43	44	38.6	694	2	US-08-816-977-49	Sequence 49, Appli
44	44	38.6	694	2	US-09-334-477-49	Sequence 49, Appli
45	44	38.6	711	2	US-08-816-977-35	Sequence 35, Appli

ALIGNMENTS

RESULT 1

US-07-988-430-58
; Sequence 58, Application US/07988430
; Patent No. 5416202
; GENERAL INFORMATION:
; APPLICANT: Bernhardt, Susan L.
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen P.
; APPLICANT: Lane, Julie A.
; APPLICANT: Lei, Shau-Ping
; TITLE OF INVENTION: Materials Comprising and Methods of
; TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/988,430
; FILING DATE: 19921209
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5416202and, Greta E.
; REGISTRATION NUMBER: 35302
; REFERENCE/DOCKET NUMBER: 31133
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear

MOLECULE TYPE: peptide
US-07-988-430-58

Query Match 100.0%; Score 114; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHSRVARMSDEFPSSMC 20
Db 1 CHHHSRVARMSDEFPSSMC 20

RESULT 2

US-08-425-336-56
; Sequence 56, Application US/08425336
; Patent No. 5621083
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425,336
; FILING DATE: 18-APR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Thomas C.
; REGISTRATION NUMBER: P-36,989
; REFERENCE/DOCKET NUMBER: 31394
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-425-336-56

Query Match 100.0%; Score 114; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHSRVARMSDEFPSSMC 20
Db 1 CHHHSRVARMSDEFPSSMC 20

RESULT 3

US-08-488-113B-56
; Sequence 56, Application US/08488113B
; Patent No. 5744580
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,113B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-488-113B-56

Query Match 100.0%; Score 114; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHSRVARMSDEFPSSMC 20
Db 1 CHHHSRVARMSDEFPSSMC 20

RESULT 4

US-08-477-484B-56
; Sequence 56, Application US/08477484B
; Patent No. 5756699
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.

;; APPLICANT: Studnika, Gary M.
;; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;; TITLE OF INVENTION: Proteins
;; NUMBER OF SEQUENCES: 169
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;; STREET: 500 West Madison Street, 34th floor
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: USA
;; ZIP: 60661
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/477,484B
;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/425,336
;; FILING DATE: 18-APR-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/064,691
;; FILING DATE: 12-MAY-1993
;; APPLICATION NUMBER: US 07/988,430
;; FILING DATE: 09-DEC-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/901,707
;; FILING DATE: 19-JUN-1992
;; APPLICATION NUMBER: US 07/787,567
;; FILING DATE: 04-NOV-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: McNicholas, Janet M.
;; REGISTRATION NUMBER: 32,918
;; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312/707-8889
;; TELEFAX: 312/707-9155
;; TELEX: 650 388-1248
;; INFORMATION FOR SEQ ID NO: 56:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-08-477-484B-56

Query Match 100.0%; Score 114; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHSRVARMSDEFPFSC 20
Db 1 CHHHSRVARMSDEFPFSC 20

RESULT 5
US-08-646-360-56
Sequence 56, Application US/08646360
Patent No. 5837491
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.

;; STREET: 500 West Madison Street, 34th floor
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: USA
;; ZIP: 60661
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/646,360
;; FILING DATE: 13-MAY-1996
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US94/05348
;; FILING DATE: 12-MAY-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/064,691
;; FILING DATE: 12-MAY-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/988,430
;; FILING DATE: 09-DEC-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/901,707
;; FILING DATE: 19-JUN-1992
;; APPLICATION NUMBER: US 07/787,567
;; FILING DATE: 04-NOV-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: McNicholas, Janet M.
;; REGISTRATION NUMBER: 32,918
;; REFERENCE/DOCKET NUMBER: 200-70.P4
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312/707-8889
;; TELEFAX: 312/707-9155
;; TELEX: 650 388-1248
;; INFORMATION FOR SEQ ID NO: 56:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-08-646-360-56

Query Match 100.0%; Score 114; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHSRVARMSDEFPFSC 20
Db 1 CHHHSRVARMSDEFPFSC 20

RESULT 6
US-08-839-765-56
Sequence 56, Application US/08839765
Patent No. 6146631
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:


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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/839,765
; FILING DATE: 15-APR-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-839-765-56
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Query Match 100.0%; Score 114; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 CHHHSRVARMSDEFFPSMC 20
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RESULT 7
US-09-136-389-56
; Sequence 56, Application US/09136389
; Patent No. 6146850
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/136,389
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; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-136-389-56
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Query Match 100.0%; Score 114; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 CHHHSRVARMSDEFFPSMC 20
Db 1 CHHHSRVARMSDEFFPSMC 20
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RESULT 8
US-09-610-838-56
; Sequence 56, Application US/09610838
; Patent No. 6376217
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/610,838
; FILING DATE: 06-JUL-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/136,389
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; FILING DATE: 18-AUG-1998
; APPLICATION NUMBER: 08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-610-838-56

Query Match 100.0%; Score 114; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHSRVARMSDEFPFPMC 20
Db 1 CHHHSRVARMSDEFPFPMC 20

RESULT 9
US-09-711-485-56
; Sequence 56, Application US/09711485
; Patent No. 6649742
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/711.485
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/839,765
; FILING DATE:
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-711-485-56

Query Match 100.0%; Score 114; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHSRVARMSDEFPFPMC 20
Db 1 CHHHSRVARMSDEFPFPMC 20

RESULT 10
PCT-US92-09487-58
; Sequence 58, Application PC/TUS9209487
; GENERAL INFORMATION:
; APPLICANT: Bernhard, Susan L.
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Lane, Julie A.
; APPLICANT: Lei, Shau-Ping
; TITLE OF INVENTION: Materials Comprising and Methods of
; TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/09487
; FILING DATE: 19921104
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:


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;; NAME: Noland, Greta E.
;; REGISTRATION NUMBER: 35302
;; REFERENCE/DOCKET NUMBER: 31133
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (312) 346-5750
;; TELEFAX: (312) 984-9740
;; TELEX: 25-3856
;; INFORMATION FOR SEQ ID NO: 58:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20 amino acids
;; TYPE: AMINO ACID
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
PCT-US92-09487-58

Query Match 100.0%; Score 114; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHSRVARVASDEFPSC 20
Db 1 CHHHSRVARVASDEFPSC 20

RESULT 11
US-08-378-761A-73
; Sequence 73, Application US/08378761A
; Patent No. 5635384
; GENERAL INFORMATION:
; APPLICANT: WALSH, TERENCE A
; APPLICANT: HEY, TIMOTHY D
; APPLICANT: MORGAN, ALICE ER
; TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
; TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ANDREA T. BORUCKI
; STREET: 9330 ZIONSVILLE ROAD
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: US
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/378,761A
; FILING DATE: 26-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BORUCKI, ANDREA T
; REGISTRATION NUMBER: 33651
; REFERENCE/DOCKET NUMBER: 38272B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 337-4846
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 315 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-378-761A-73

Query Match 100.0%; Score 114; DB 1; Length 315;
Best Local Similarity 100.0%; Pred. No. 5.5e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHSRVARVASDEFPSC 20
Db 1 CHHHSRVARVASDEFPSC 20

RESULT 12
US-08-485-286-73
; Sequence 73, Application US/08485286
; Patent No. 5646026
; Patent No. 5646026 5646119
; GENERAL INFORMATION:
; APPLICANT: WALSH, TERENCE A
; APPLICANT: HEY, TIMOTHY D
; APPLICANT: MORGAN, ALICE ER
; TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
; TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ANDREA T. BORUCKI
; STREET: 9330 ZIONSVILLE ROAD
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: US
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,286
; FILING DATE: 26-JAN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/378761
; FILING DATE: 26-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BORUCKI, ANDREA T
; REGISTRATION NUMBER: 33651
; REFERENCE/DOCKET NUMBER: 38272B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 337-4846
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 315 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-485-286-73

Query Match 100.0%; Score 114; DB 1; Length 315;
Best Local Similarity 100.0%; Pred. No. 5.5e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHSRVARVASDEFPSC 20
Db 264 CHHHSRVARVASDEFPSC 283

RESULT 13
US-08-816-977-2
; Sequence 2, Application US/08816977
; Patent No. 6080400
; GENERAL INFORMATION:
; APPLICANT: Williams, James A.
; APPLICANT: Byrnie, Lisa M.
; APPLICANT: Pugh, Charles S.G.
; TITLE OF INVENTION: Prevention And Treatment Of
; TITLE OF INVENTION: Verotoxin-Induced Disease
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
```


CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/816,977
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: OPHD-02450
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 315 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-816-977-2

Query Match 100.0%; Score 114; DB 2; Length 315;
Best Local Similarity 100.0%; Pred. No. 5.5e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHSRVARMASDEFFSMC 20
Db 264 CHHHSRVARMASDEFFSMC 283

RESULT 14
US-09-334-477-2
Sequence 2, Application US/09334477
Patent No. 6652857
GENERAL INFORMATION:
APPLICANT: Williams, James A.
Byrne, Lisa M.
Pugh, Charles S.G.
TITLE OF INVENTION: Prevention And Treatment Of
Verotoxin-Induced Disease
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/334,477
FILING DATE: 16-Jun-1999
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/816,977
FILING DATE: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: OPHD-02450
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 315 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-334-477-2

Query Match 100.0%; Score 114; DB 2; Length 315;
Best Local Similarity 100.0%; Pred. No. 5.5e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHSRVARMASDEFFSMC 20
Db 264 CHHHSRVARMASDEFFSMC 283

RESULT 15
US-08-816-977-21
Sequence 21, Application US/08816977
Patent No. 6080400
GENERAL INFORMATION:
APPLICANT: Williams, James A.
APPLICANT: Byrne, Lisa M.
APPLICANT: Pugh, Charles S.G.
TITLE OF INVENTION: Prevention And Treatment Of
Verotoxin-Induced Disease
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/816,977
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: OPHD-02450
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 323 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-816-977-21

Query Match 100.0%; Score 114; DB 2; Length 323;
Best Local Similarity 100.0%; Pred. No. 5.6e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHSRVARMASDEFFSMC 20
Db 264 CHHHSRVARMASDEFFSMC 283

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OM protein - protein search, using sw model

Run on: February 10, 2006, 10:37:59 ; Search time 13.0627 Seconds
(without alignments)
639.727 Million cell updates/sec

Title: US-10-717-243-56

Perfect score: 114

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Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	114	100.0	20	5	US-10-717-243-56
3	114	100.0	293	3	US-09-792-793A-37
4	114	100.0	293	4	US-10-375-209A-37
5	114	100.0	315	3	US-09-334-477-2
6	114	100.0	323	3	US-09-334-477-21
7	114	100.0	326	3	US-09-334-477-37
8	114	100.0	332	3	US-09-765-527-251
9	114	100.0	690	3	US-09-334-477-47
10	114	100.0	708	3	US-09-334-477-33
11	48	42.1	96	4	US-10-425-115-237717
12	48	42.1	162	4	US-10-767-701-40168
13	47	41.2	74	4	US-10-424-599-224605
14	47	41.2	135	3	US-09-962-021-3
15	47	41.2	135	4	US-10-408-765A-20
16	47	41.2	293	5	US-10-732-923-4254
17	47	41.2	294	4	US-10-437-963-194718
18	46.5	40.8	345	4	US-10-424-599-200140
19	46	40.4	19	5	US-10-502-882-10
20	46	40.4	196	4	US-10-282-122A-66424
21	45	39.5	380	4	US-10-437-963-116579
22	44.5	39.0	250	4	US-10-369-493-10325
23	44.5	39.0	275	4	US-10-425-115-220907
24	44.5	39.0	280	4	US-10-425-114-52863
25	44.5	39.0	544	3	US-09-925-299-1004
26	44.5	39.0	544	3	US-09-925-299-1004
27	44	38.6	82	4	US-10-424-599-216625

28 44 38.6 137 4 US-10-408-765A-1100 Sequence 1100, Ap
29 44 38.6 138 3 US-09-962-021-1 Sequence 1, Appli
30 44 38.6 249 4 US-10-156-761-13851 Sequence 13851, A
31 44 38.6 286 5 US-10-732-923-14451 Sequence 14451, A
32 44 38.6 293 4 US-10-424-599-223435 Sequence 223435,
33 44 38.6 318 3 US-09-334-477-6 Sequence 6, Appli
34 44 38.6 319 3 US-09-792-793A-38 Sequence 38, Appl
35 44 38.6 319 3 US-09-870-759-28 Sequence 28, Appl
36 44 38.6 319 3 US-09-751-708A-28 Sequence 28, Appl
37 44 38.6 319 4 US-10-375-209A-38 Sequence 38, Appl
38 44 38.6 319 4 US-10-428-817A-24 Sequence 24, Appl
39 44 38.6 319 5 US-10-937-758A-28 Sequence 28, Appl
40 44 38.6 326 3 US-10-503-415-2 Sequence 2, Appli
41 44 38.6 326 3 US-09-334-477-25 Sequence 25, Appl
42 44 38.6 427 4 US-09-334-477-39 Sequence 39, Appl
43 44 38.6 427 4 US-10-437-963-106648 Sequence 106648,
44 44 38.6 433 3 US-09-344-882-26 Sequence 26, Appl
45 44 38.6 433 4 US-10-293-865-26 Sequence 26, Appl

ALIGNMENTS

RESULT 1

US-10-127-890-56
; Sequence 56, Application US/10127890
; Publication No. US20030166196A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Cartoli, Stephen F.
; Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/127,890
; FILING DATE: 23-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/POCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:

Byrne, Lisa M.
Pugh, Charles S.G.
TITLE OF INVENTION: Prevention And Treatment Of
Verotoxin-Induced Disease
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/334,477
FILING DATE: 16-Jun-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/816,977
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: OPHD-02450
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 315 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-334-477-2
Query Match 100.0%; Score 114; DB 3; Length 315;
Best Local Similarity 100.0%; Pred. No. 1.8e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CHHHSRVARWASDEFFSMC 20
Db 264 CHHHSRVARWASDEFFSMC 283
RESULT 6
US-09-334-477-21
Sequence 21, Application US/09334477
Patent No. US20020012658A1
GENERAL INFORMATION:
APPLICANT: Williams, James A.
Byrne, Lisa M.
Pugh, Charles S.G.
TITLE OF INVENTION: Prevention And Treatment Of
Verotoxin-Induced Disease
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/334,477
FILING DATE: 16-Jun-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/816,977
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: OPHD-02450
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 323 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-334-477-21
Query Match 100.0%; Score 114; DB 3; Length 323;
Best Local Similarity 100.0%; Pred. No. 1.9e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CHHHSRVARWASDEFFSMC 20
Db 264 CHHHSRVARWASDEFFSMC 283
RESULT 7
US-09-334-477-37
Sequence 37, Application US/09334477
Patent No. US20020012658A1
GENERAL INFORMATION:
APPLICANT: Williams, James A.
Byrne, Lisa M.
Pugh, Charles S.G.
TITLE OF INVENTION: Prevention And Treatment Of
Verotoxin-Induced Disease
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/334,477
FILING DATE: 16-Jun-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/816,977
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: OPHD-02450
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 327 amino acids
TYPE: amino acid
TOPOLOGY: linear


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; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-09-334-477-37

Query Match          100.0%; Score 114; DB 3; Length 326;
Best Local Similarity 100.0%; Pred. No. 1.9e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHSRVARVMSDEFPFSC 20
Db 275 CHHHSRVARVMSDEFPFSC 294

RESULT 8
US-09-765-527-251
; Sequence 251, Application US/09765527
; Patent No. US20020006638A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; Fusion Proteins and BPI-Derived Peptides
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,527
; FILING DATE: 18-Jan-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/621,803
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 251:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 332 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 251:
US-09-765-527-251

Query Match          100.0%; Score 114; DB 3; Length 332;
Best Local Similarity 100.0%; Pred. No. 1.9e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHSRVARVMSDEFPFSC 20
Db 277 CHHHSRVARVMSDEFPFSC 296

RESULT 9
US-09-334-477-47
; Sequence 47, Application US/09334477
; Patent No. US2002012658A1
; GENERAL INFORMATION:
; APPLICANT: Williams, James A.
; BYRNE, Lisa M.
; PUGH, Charles S.G.
; TITLE OF INVENTION: Prevention And Treatment Of
; Verotoxin-Induced Disease
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/334,477
; FILING DATE: 16-Jun-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/816,977
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: OPHD-02450
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 690 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-09-334-477-47

Query Match          100.0%; Score 114; DB 3; Length 690;
Best Local Similarity 100.0%; Pred. No. 4.2e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHSRVARVMSDEFPFSC 20
Db 639 CHHHSRVARVMSDEFPFSC 658

RESULT 10
US-09-334-477-33
; Sequence 33, Application US/09334477
; Patent No. US2002012658A1
; GENERAL INFORMATION:
; APPLICANT: Williams, James A.
; BYRNE, Lisa M.
; PUGH, Charles S.G.
; TITLE OF INVENTION: Prevention And Treatment Of
; Verotoxin-Induced Disease
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/334,477
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; FILING DATE: 16-Jun-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/816,977
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: OPD-02450
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 709 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-09-334-477-33

Query Match 100.0%; Score 114; DB 3; Length 708;
Best Local Similarity 100.0%; Pred. No. 4.3e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHSRVARMASDEFPSC 20
Db 657 CHHHSRVARMASDEFPSC 676

RESULT 11
US-10-425-115-237717
; Sequence 237717, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 237717
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_148383C.1.pep
US-10-425-115-237717

Query Match 42.1%; Score 48; DB 4; Length 96;
Best Local Similarity 50.0%; Pred. NO. 11;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CHHHSRVARMASD 14
Db 82 CHHHLRSLGSAID 95

RESULT 12
US-10-767-701-40168
; Sequence 40168, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B

; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 40168
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C46914_1.pep
US-10-767-701-40168

Query Match 42.1%; Score 48; DB 4; Length 162;
Best Local Similarity 44.4%; Pred. No. 19;
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CHHHSRVARMASDEFPSS 18
Db 44 CYHHHDNYATVSTDFFS 61

RESULT 13
US-10-424-599-224605
; Sequence 224605, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 224605
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_44849C.1.pep
US-10-424-599-224605

Query Match 41.2%; Score 47; DB 4; Length 74;
Best Local Similarity 50.0%; Pred. No. 12;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 2 HHHSRVARMASDEFP 17
Db 58 HGHGSKVSTLASSNFP 73

RESULT 14
US-09-962-021-3
; Sequence 3, Application US/09962021
; Patent No. US20020106737A1
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: HUMAN SOM1 PROTEIN HOMOLOG
; FILE REFERENCE: PF-0170-2 CON
; CURRENT APPLICATION NUMBER: US/09/962,021
; CURRENT FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PERL Program
; SEQ ID NO 3
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020106737A1 g180233
US-09-962-021-3

Query Match 41.2%; Score 47; DB 3; Length 135;
Best Local Similarity 44.4%; Pred. No. 22;
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 CHHHSRVARMSDEFFS 18
| | | | | : | | | |
Db 58 CAHLIRLLKCKRDSFPS 75

RESULT 15
US-10-408-765A-20
; Sequence 20, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 60088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-20

Query Match 41.2%; Score 47; DB 4; Length 135;
Best Local Similarity 44.4%; Pred. No. 22;
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 CHHHSRVARMSDEFFS 18
| | | | | : | | | |
Db 58 CAHLIRLLKCKRDSFPS 75

Search completed: February 10, 2006, 10:44:46
Job time : 14.0627 secs

GenCore version 5.1.7

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OM protein - protein search, using sw model

Run on: February 10, 2006, 10:39:04 ; Search time 1.03321 Seconds
(without alignments)
254.015 Million cell updates/sec

Title: US-10-717-243-56

Perfect score: 114

Sequence: 1 CHHHSRVARWASDEFFSMC 20

Scoring table: BLOSUM62

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Searched: 97014 seqs, 13122538 residues

Total number of hits satisfying chosen parameters: 97014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA-New:

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3: /cgm2_6/ptodata/1/pubaa/US07_NEW_PUB.pep.*
4: /cgm2_6/ptodata/1/pubaa/PTCT_NEW_PUB.pep.*
5: /cgm2_6/ptodata/1/pubaa/US09_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	114	100.0	315	7	US-11-010-795-28
2	44	38.6	319	7	US-11-010-795-26
3	44	38.6	433	7	US-11-167-856-26
4	43	37.7	541	7	US-11-059-814-20
5	40	35.1	493	7	US-11-010-239-81
6	39	34.2	205	6	US-10-793-626-1828
7	39	34.2	263	6	US-10-793-626-1418
8	39	34.2	285	7	US-11-094-519A-36
9	39	34.2	399	7	US-11-094-519A-37
10	39	34.2	402	6	US-10-821-234-1581
11	39	34.2	502	7	US-11-111-664-6
12	39	34.2	512	7	US-11-111-664-8
13	38	33.3	304	6	US-10-793-626-1530
14	38	33.3	423	6	US-10-883-512-76
15	38	33.3	559	6	US-10-521-162-4
16	38	33.3	699	7	US-11-138-882-4
17	38	33.3	699	7	US-11-138-882-4
18	38	33.3	712	6	US-10-521-162-12
19	37.5	32.9	244	6	US-10-467-657-2638
20	37	32.5	146	7	US-11-226-657-63
21	37	32.5	259	7	US-11-156-084-326
22	37	32.5	306	7	US-11-152-569-19
23	37	32.5	486	6	US-10-877-346-50
24	37	32.5	569	6	US-10-632-150-2
25	37	32.5	569	7	US-11-073-457-2

26 37 32.5 569 7 US-11-039-691-12 Sequence 12, Appl
27 37 32.5 569 7 US-11-073-460-2 Sequence 2, Appl
28 37 32.5 798 7 US-11-107-028-3 Sequence 3, Appl
29 37 32.5 954 6 US-10-453-372-1150 Sequence 1150, Ap
30 37 32.5 1189 6 US-10-821-234-1209 Sequence 1209, Ap
31 37 32.5 1268 6 US-10-453-372-1144 Sequence 1144, Ap
32 37 32.5 1268 6 US-10-453-372-1154 Sequence 1154, Ap
33 37 32.5 1288 6 US-10-453-372-1146 Sequence 1146, Ap
34 37 32.5 1288 6 US-10-453-372-1152 Sequence 1152, Ap
35 37 32.5 1766 7 US-11-075-185-10 Sequence 10, Appl
36 36 31.6 19 6 US-10-939-890-241 Sequence 241, App
37 36 31.6 227 7 US-11-052-564A-319 Sequence 319, App
38 36 31.6 277 6 US-10-467-657-2886 Sequence 2886, Ap
39 36 31.6 419 7 US-11-166-993-147 Sequence 147, App
40 36 31.6 604 7 US-11-183-136-4 Sequence 4, Appl
41 36 31.6 604 7 US-11-046-653-1 Sequence 1, Appl
42 36 31.6 832 7 US-11-182-016-8 Sequence 8, Appl
43 36 31.6 1017 7 US-11-054-281-108 Sequence 108, App
44 36 31.6 1219 7 US-11-054-281-28 Sequence 28, Appl
45 36 31.6 1219 7 US-11-054-281-106 Sequence 106, App

ALIGNMENTS

RESULT 1

US-11-010-795-28
; Sequence 28, Application US/11010795
; Publication No: US20060005271A1
; GENERAL INFORMATION:
; APPLICANT: TUMER, NILGUN E.
; APPLICANT: DI, RONG
; TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING L3 DELTA PROTEINS ARE
; FILE REFERENCE: OCIRS 3.0-085
; CURRENT APPLICATION NUMBER: US/11/010,795
; CURRENT FILING DATE: 2004-12-13
; PRIOR FILING DATE: 2003-12-12
; PRIOR FILING DATE: 2003-12-12
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 28
; TYPE: PRT
; LENGTH: 315
; ORGANISM: Bacteriophage SC370
US-11-010-795-28

Query Match 100.0%; Score 114; DB 7; Length 315;
Best Local Similarity 100.0%; Pred. No. 2.2e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHSRVARWASDEFFSMC 20
Db 264 CHHHSRVARWASDEFFSMC 283

RESULT 2

US-11-010-795-26
; Sequence 26, Application US/11010795
; Publication No: US20060005271A1
; GENERAL INFORMATION:
; APPLICANT: TUMER, NILGUN E.
; APPLICANT: DI, RONG
; TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING L3 DELTA PROTEINS ARE
; FILE REFERENCE: OCIRS 3.0-085
; CURRENT APPLICATION NUMBER: US/11/010,795
; CURRENT FILING DATE: 2004-12-13
; PRIOR FILING DATE: 2003-12-12
; PRIOR FILING DATE: 2003-12-12
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 26

; LENGTH: 205
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-1828

Query Match 34.2%; Score 39; DB 6; Length 205;
Best Local Similarity 57.1%; Pred. No. 20;
Matches 8; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 HHASRVARMASDEF 16
Db 19 HHGKAVRGASDTF 32
||| ||| |||

RESULT 7
US-10-793-626-1418
; Sequence 1418, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMBERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PUS480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1418
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-1418

Query Match 34.2%; Score 39; DB 6; Length 263;
Best Local Similarity 57.1%; Pred. No. 26;
Matches 8; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 HHASRVARMASDEF 16
Db 56 HHGKAVRGASDTF 69
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RESULT 8
US-11-094-519A-36
; Sequence 36, Application US/11094519A
; Publication No. US20050281810A1
; GENERAL INFORMATION:
; APPLICANT: BERNSTEIN, Jeanne
; APPLICANT: LEVINE, Zurit
; TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING
; FILE REFERENCE: 2786-0140P
; CURRENT APPLICATION NUMBER: US/11/094,519A
; CURRENT FILING DATE: 2005-03-31
; PRIOR APPLICATION NUMBER: US/09/695,293
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: IL 132558
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 36
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-094-519A-36

Query Match 34.2%; Score 39; DB 7; Length 285;

Best Local Similarity 61.5%; Pred. No. 28;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 HHASRVARMASD 14
Db 25 HHPPSYVAHLASD 37
||| ||| |||

RESULT 9
US-11-094-519A-37
; Sequence 37, Application US/11094519A
; Publication No. US20050281810A1
; GENERAL INFORMATION:
; APPLICANT: BERNSTEIN, Jeanne
; APPLICANT: LEVINE, Zurit
; TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING
; FILE REFERENCE: 2786-0140P
; CURRENT APPLICATION NUMBER: US/11/094,519A
; CURRENT FILING DATE: 2005-03-31
; PRIOR APPLICATION NUMBER: US/09/695,293
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: IL 132558
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 37
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-094-519A-37

Query Match 34.2%; Score 39; DB 7; Length 399;
Best Local Similarity 61.5%; Pred. No. 39;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 HHASRVARMASD 14
Db 25 HHPPSYVAHLASD 37
||| ||| |||

RESULT 10
US-10-821-234-1581
; Sequence 1581, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: PT_SEQ_genes Version 1.0
; SEQ ID NO 1581
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1581

Query Match 34.2%; Score 39; DB 6; Length 402;
Best Local Similarity 61.5%; Pred. No. 39;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 HHASRVARMASD 14
Db 25 HHPPSYVAHLASD 37
||| ||| |||

RESULT 11

; TITLE OF INVENTION: FLEA AND TICK OCTOPAMINE RECEPTOR NUCLEIC ACID MOLECULES,
; FILE REFERENCE: FC-11-PCT
; CURRENT APPLICATION NUMBER: US/10/521,162
; PRIOR FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: 60/319,402
; PRIOR FILING DATE: 2003-07-17
; PRIOR APPLICATION NUMBER: 60/426,601
; PRIOR FILING DATE: 2003-11-15
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 559
; TYPE: PRT
; ORGANISM: Ctenocephalides felis
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (192)..(192)
; OTHER INFORMATION: The 'Xaa' at location 192 stands for Ala, or Thr.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (193)..(193)
; OTHER INFORMATION: The 'Xaa' at location 193 stands for Asn, or Tyr.
US-10-521-162-4

Query Match 33.3%; Score 38; DB 6; Length 559;
Best Local Similarity 83.3%; Pred. No. 79;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHS 6
Db 140 CHHSS 145

Search completed: February 10, 2006, 10:45:19
Job time : 1.03321 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 10, 2006, 09:56:49 ; Search time 10.8856 Seconds
(without alignments)
807.265 Million cell updates/sec

Title: US-10-717-243-57

Perfect score: 100

Sequence: 1 PSCQAGAAASELFSINAY 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_21:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	100	100.0	20	2 AAR37301	Aar37301 Rabbit Mu
2	99	99.0	153	5 ABP42706	Abp42706 Human ova
3	99	99.0	363	2 RAY07116	Ray07116 Lung canc
4	99	99.0	364	2 RAY06992	Ray06992 Glycolyti
5	99	99.0	364	7 ADF76857	Adf76857 Novel hum
6	99	99.0	364	7 ADJ68731	Adj68731 Human hea
7	99	99.0	364	8 ADE77178	Ade77178 Human pro
8	99	99.0	364	8 ADI02918	Adi02918 Human fru
9	99	99.0	364	8 ADQ76754	Adq76754 Human fru
10	99	99.0	364	8 AEM81754	Aem81754 Tumour-as
11	99	99.0	364	8 ADU46860	Adu46860 Aldolase
12	99	99.0	364	9 ADX05876	Adx05876 Cyclin-de
13	99	99.0	364	9 ADZ70640	Adz70640 Human pro
14	99	99.0	364	9 ADZ70327	Adz70327 Human pro
15	97	97.0	22	9 ADV50900	Adv50900 Murine br
16	97	97.0	364	7 ADE79827	Ade79827 Rat aldol
17	95	95.0	31	3 AAB44017	Aab44017 Human can
18	68	68.0	363	9 ADW08677	Adw08677 Human pro
19	68	68.0	364	5 ABP65148	Abp65148 Hypoxia-r
20	68	68.0	364	7 ADJ68292	Adj68292 Human hea
21	68	68.0	364	8 ADL12661	Adl12661 Human ste
22	61	61.0	365	8 ADN23270	Adn23270 Bacterial
23	55.5	55.5	361	4 ABB66969	Abb66969 Drosophil
24	52	52.0	366	8 ADN23082	Adn23082 Bacterial

ALIGNMENTS

RESULT 1

AAR37301

ID AAR37301 standard; protein; 20 AA.

XX

AC AAR37301;

XX

DT 25-MAR-2003 (revised)

DT 13-SEP-1993 (first entry)

XX

XX

DE Rabbit Muscle aldolase peptide segment.

XX

KW Type I ribosome-inactivating protein; ricin; momordin; immunoconjugate;

KW autoimmune disease; cell killing; toxin; human engineered antibody;

KW variable region; light chain; cell targeting; chimeric antibody; RMA;

KW linker.

XX

OS Oryctolagus cuniculus.

XX

FH Key Location/Qualifiers

FT Cleavage-site 1..20

FT /note= "contains several potential cathepsin cleavage

FT sites"

XX

XX WO9309130-A1.

XX

PD 13-MAY-1993.

XX

XX

PF 04-NOV-1992; 92WO-US009487.

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PR 04-NOV-1991; 91US-00787567.

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25 51 51.0 371 8 ADY10167
26 50.5 50.5 215 8 ABO60233
27 50.5 50.5 836 7 ABR83671
28 50.5 50.5 836 7 ADM05015
29 50.5 50.5 836 8 ADO85827
30 48 48.0 1772 8 ADR12606
31 47 47.0 1223 4 ABB63399
32 46 46.0 9 8 ADN63558
33 46 46.0 132 6 ABP96323
34 46 46.0 171 9 AEA59099
35 46 46.0 170 6 ABU01993
36 46 46.0 170 8 ADK46838
37 46 46.0 171 8 ADR95229
38 46 46.0 283 4 AAM93735
39 46 46.0 283 8 ADL31668
40 46 46.0 292 6 AAO19583
41 46 46.0 292 6 ABB99461
42 46 46.0 295 6 AAO19582
43 46 46.0 295 8 ADR10068
44 46 46.0 324 5 ABP69378
45 46 46.0 324 5 ABP69378

Ady10167 Plant ful
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Abr83671 Human bkl
Adm05015 Human pro
Ado85827 Different
Adr12606 Gene vacc
Abb63399 Drosophil
Adn63558 HLA bindi
Abp96323 Human AGE
Adm64270 HLA bindi
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Adr95229 Novel S.
Aea59099 Streptoco
Aam93735 Human pol
Ad

CC specifically binds to a target cell. Pref. target-cell binding molecules
 CC are antibodies or their fragments, esp. human engineered H65 antibody
 CC fragments. Fusion constructs were assembled that included a natural
 CC sequence gelonin gene fused to an H65 truncated heavy chain gene or an
 CC H65 light chain (kappa) gene. A DNA linker encoding a peptide segment of
 CC the rabbit muscle aldolase was inserted between the gelonin gene and the
 CC Ab gene. The resulting immunoconjugates can be used as cytotoxic
 CC therapeutic agents. (Updated on 25-MAR-2003 to correct FN field.)
 XX
 SQ Sequence 20 AA;
 Query Match 100.0%; Score 100; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 9.4e-10; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 PSGQAGAAASESLFISNHAY 20
 Db 1 PSGQAGAAASESLFISNHAY 20
 RESULT 2
 ID ABP42706 standard; protein; 153 AA.
 AC ABP42706;
 XX
 XX 22-AUG-2002 (first entry)
 DT
 XX Human ovarian antigen HOPKN14, SEQ ID NO:3838.
 DE
 XX Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
 KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
 KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
 KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
 KW inflammatory condition; immune disorder; blood disorder;
 KW cardiovascular disorder; respiratory disorder; neurological disorder;
 KW gastrointestinal disorder; urinary system disorder; drug screening;
 KW gene therapy; chromosome mapping; forensic analysis;
 KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
 KW antiinflammatory; gynaecological; reproductive.
 XX
 OS Homo sapiens.
 XX
 XX WO200200677-A1.
 FN
 XX 03-JAN-2002.
 PD
 XX 07-JUN-2001; 2001WO-US018569.
 PP
 XX 07-JUN-2000; 2000US-0209467P.
 PR
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX Birse CE, Rosen CA;
 PI
 XX WPI; 2002-147878/19.
 DR
 XX N-PSDB; ABQ55783.
 DR
 XX Isolated nucleic acid molecules encoding novel ovarian polypeptides,
 PT useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian
 PT cancer), immune disorders, cardiovascular disorders and neurological
 PT diseases.
 PT
 XX Claim 11; SEQ ID NO 3838; 2922pp; English.
 PS
 XX The invention relates to 2175 novel human ovarian antigens (ABP41054-
 CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
 CC encompasses polypeptides 90% identical and polynucleotides 95% identical
 CC to the sequences of the invention. The invention additionally relates to
 CC recombinant vectors and host cells comprising human ovarian antigen
 CC polynucleotides, antibodies against human ovarian antigens, and the use
 CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
 CC treating, prognosing or preventing various ovary and/or breast-related

CC disorders. Such conditions include ovarian cancer and breast cancer, and
 CC metastatic tumours of ovarian or breast origin, reproductive system
 CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
 CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
 CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
 CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
 CC vaginitis), immune disorders (e.g., congenital and acquired
 CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
 CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
 CC respiratory disorders, neurological disorders, gastrointestinal disorders
 CC and urinary system disorders. Ovarian antigen polypeptides and
 CC polynucleotides may also be used in screening for compounds which
 CC modulate ovarian antigen expression or activity. The polynucleotides may
 CC further be used for gene therapy, chromosome mapping, in the
 CC identification of individuals and in forensic analysis, and the
 CC polypeptides may be used as food additives or to prepare antibodies
 CC useful in disease diagnosis, drug targeting and phenotyping. The present
 CC sequence represents a human ovarian antigen of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 CC
 XX SQ Sequence 153 AA;
 Query Match 99.0%; Score 99; DB 5; Length 153;
 Best Local Similarity 95.0%; Pred. No. 1.5e-08;
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 PSGQAGAAASESLFISNHAY 20
 Db 134 PSGQAGAAASESLFVSNHAY 153
 RESULT 3
 AAY07116
 ID AAY07116 standard; protein; 363 AA.
 XX
 AC AAY07116;
 XX
 XX 02-JUL-1999 (first entry)
 DT
 XX Lung cancer associated antigen precursor sequence.
 DE
 XX Cancer associated antigen; diagnosis; research; treatment; human;
 KW breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer;
 KW prostate cancer.
 KW
 XX Homo sapiens.
 OS
 XX WO9904265-A2.
 FN
 XX 28-JAN-1999.
 PD
 XX 15-JUL-1998; 98WO-US014679.
 PP
 XX 17-JUL-1997; 97US-00896164.
 PR
 XX 10-OCT-1997; 97US-0061599P.
 PR
 XX 10-OCT-1997; 97US-0061765P.
 PR
 XX 10-OCT-1997; 97US-00948705.
 PR
 XX 11-OCT-1997; 97GB-00021697.
 PR
 XX 22-JUN-1998; 98US-00102322.
 PR
 XX (LUDW-) LUDWIG INST CANCER RES.
 PA
 XX Old LJ, Scanlan MJ, Stockert E, Gure A, Chen Y, Gout I;
 PI O'hare M, Obata Y, Pfreundschuh M, Tureci O, Sahin U;
 XX WPI; 1999-132448/11.
 DR
 XX New isolated cancer associated nucleic acids and polypeptides - isolated
 PT using sera from cancer patients, used to develop products for the
 PT diagnosis, monitoring or treatment of cancers.
 PT
 XX

PS Disclosure; Page 733-734; 787pp; English.

XX The invention relates to a method for diagnosing a disorder characterised
 CC by expression of a human cancer associated antigen precursor coded for by
 CC a nucleic acid molecule (NAM). The method comprises: (a) contacting a
 CC biological sample isolated from a subject with an agent that specifically
 CC binds to the NAM, an expression product or a fragment of an expression
 CC product complexed with an HLA molecule; and (b) determining the
 CC interaction between the agent and the NAM or the expression product as a
 CC determination of the disorder. The products and methods can be used in
 CC the diagnosis, monitoring, research, or treatment of conditions
 CC characterised by the expression of various cancer associated antigens.
 CC The invention provides nucleic acid sequences and encoded polypeptides
 CC which are cancer associated antigen precursors expressed in human breast
 CC cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and
 CC lung cancer

XX Sequence 363 AA;

Query Match 99.0%; Score 99; DB 2; Length 363;
 Best Local Similarity 95.0%; Pred. No. 4.2e-08;
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSGQAGAAASESLFVSNHAY 20

Db 344 PSGQAGAAASESLFVSNHAY 363

RESULT 4

AA06992
 ID AA06992 standard; protein; 364 AA.

AC AA06992;

DT 02-JUL-1999 (first entry)

DE Glycolytic enzyme aldolase A.

KW Cancer associated antigen; diagnosis; research; treatment; human;
 KW breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer;
 KW prostate cancer.

XX Homo sapiens.

OS WO9904265-A2.

PN 28-JAN-1999.

PD 15-JUL-1998; 98WO-US014679.

PR 17-JUL-1997; 97US-00896164.

PR 10-OCT-1997; 97US-0061599P.

PR 10-OCT-1997; 97US-0061765P.

PR 10-OCT-1997; 97US-00948705.

PR 11-OCT-1997; 97GB-00021697.

PR 22-JUN-1998; 98US-00102322.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Old LJ, Scanlan MJ, Stockert E, Gure A, Chen Y, Gout I;

PI O'hare M, Obata Y, Pfreundschuh M, Tureci O, Sahin U;

XX WPI; 1999-132448/11.

DR N-PSDB; AAX40193.

XX New isolated cancer associated nucleic acids and polypeptides - isolated
 PT using sera from cancer patients, used to develop products for the
 PT diagnosis, monitoring or treatment of cancers.

XX Example 8; Page 769-770; 787pp; English.

XX The invention relates to a method for diagnosing a disorder characterised
 CC by expression of a human cancer associated antigen precursor coded for by

CC a nucleic acid molecule (NAM). The method comprises: (a) contacting a
 CC biological sample isolated from a subject with an agent that specifically
 CC binds to the NAM, an expression product or a fragment of an expression
 CC product complexed with an HLA molecule; and (b) determining the
 CC interaction between the agent and the NAM or the expression product as a
 CC determination of the disorder. The products and methods can be used in
 CC the diagnosis, monitoring, research, or treatment of conditions
 CC characterised by the expression of various cancer associated antigens.
 CC The invention provides nucleic acid sequences and encoded polypeptides
 CC which are cancer associated antigen precursors expressed in human breast
 CC cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and
 CC lung cancer

XX Sequence 364 AA;

Query Match 99.0%; Score 99; DB 2; Length 364;
 Best Local Similarity 95.0%; Pred. No. 4.2e-08;
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSGQAGAAASESLFVSNHAY 20

Db 345 PSGQAGAAASESLFVSNHAY 364

RESULT 5

ADP76857
 ID ADP76857 standard; protein; 364 AA.

AC ADP76857;

DT 26-FEB-2004 (first entry)

DE Novel human secreted and transmembrane protein SeqID 532.

KW human; PRO: membrane bound protein; membrane bound receptor;
 KW cell proliferation; cell migration; cell differentiation;
 KW mitogenic factor; survival factor; cytotoxic factor;
 KW differentiation factor; neurotrophic factor; hormone; cell receptor;
 KW receptor-ligand interaction; cytostatic; chondrocyte; tumour.

XX Homo sapiens.

XX WO2003072035-A2.

XX 04-SEP-2003.

XX 21-FEB-2003; 2003WO-US005241.

XX 22-FEB-2002; 2002US-0359461P.

XX (GETH) GENENTECH INC.

XX Bodary SC, Clark H, Hunte B, Jackman JK, Schoenfeld JR;

PI Williams FW, Wood WI, Wu TD;

XX WPI; 2003-721702/68.

DR N-PSDB; ADP76856.

XX New PRO polypeptides, useful for diagnosing and treating an immune
 PT related disorder, e.g. systemic lupus erythematosus, rheumatoid
 PT arthritis, osteoarthritis, juvenile chronic arthritis, thyroiditis or
 PT diabetes mellitus.

PS Claim 10; SEQ ID NO 532; 918pp; English.

XX This invention relates to novel nucleic acids encoding human PRO secreted
 CC and transmembrane proteins. Extracellular proteins play important roles
 CC in the formation, differentiation and maintenance of multicellular
 CC organisms. The fate of many individual cells (for example proliferation,
 CC migration or differentiation) is typically governed by information
 CC received from other cells and the immediate environment. The information
 CC is often transmitted by secreted polypeptides (for example mitogenic
 CC factors, survival factors, cytotoxic factors, differentiation factors,

CC neuropeptides and hormones) which are received and interpreted by diverse
 CC cell receptors or membrane bound proteins. These membrane bound proteins
 CC and receptors may be of use as pharmaceutical and diagnostic agents, such
 CC as in the blocking of receptor-ligand interactions. The current invention
 CC provides the amino acid sequences of novel human membrane bound receptors
 CC and proteins, along with the cDNA sequences encoding them. The novel
 CC proteins of the invention may have cytosolic activities through the
 CC stimulation of chondrocytes. The nucleic acids of the invention may be
 CC useful for the manufacture of a medicament for diagnosing or treating a
 CC tumour in a mammal. In addition, they may be useful for measuring or
 CC detecting the expression of a tumour associated gene. The present
 CC sequence is the amino acid sequence of a human PRO protein of the
 CC invention.

XX SQ Sequence 364 AA;

Query Match 99.0%; Score 99; DB 7; Length 364;
 Best Local Similarity 95.0%; Pred. No. 4.2e-08;
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 PSGQAGAAASESLFISNHAY 20
 |||||:|||||:|||||
 Db 345 PSGQAGAAASESLFVSNHAY 364

RESULT 6

ADJ68731
 ID ADJ68731 standard; protein; 364 AA.
 XX AC ADJ68731;
 XX DT 06-MAY-2004 (first entry)
 XX DE Human heat mitochondrial protein as a therapeutic target SeqIDS37.
 XX KW Mitochondrial; human; screening assay; diabetes mellitus;
 KW Huntington's disease; osteoarthritis;
 KW Leber's hereditary optic neuropathy; LHON;
 KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
 KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
 KW neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
 KW osteopathic; ophthalmological; cytosolic.
 XX OS Homo sapiens.
 XX FN WO2003087768-A2.
 XX PD 23-OCT-2003.
 XX PF 04-APR-2003; 2003WO-US010870.
 XX PR 12-APR-2002; 2002US-0372843P.
 XX PR 17-JUN-2002; 2002US-0389987P.
 XX PR 20-SEP-2002; 2002US-0412418P.
 XX (MITO-) MITOKOR.
 XX PA (BUCK-) BUCK INST AGE RES.
 XX PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
 PI Warnock DE;
 XX WPI; 2003-845369/78.

Identifying a mitochondrial target for drug screening assays and for
 treating diseases associated with altered mitochondrial function,
 comprises detecting a modified polypeptide in a sample and correlating
 with the disease.

Claim 1; SEQ ID NO 537; 180pp; English.

This invention relates to novel mitochondrial targets that can be used
 for therapeutic intervention in treating a disease associated with
 altered mitochondrial function. Specifically, it refers to a method for

CC identifying proteins of the human heart mitochondrial proteome that are
 CC useful for drug screening assays, as well as therapeutic targets. The
 CC present invention describes a method for identifying such proteins that
 CC can be used in the treatment of various diseases associated with altered
 CC mitochondrial function including diabetes mellitus, Huntington's disease,
 CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
 CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
 CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
 CC compositions have neuroprotective, nootropic, antidiabetic,
 CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
 CC cytosolic activities. This polypeptide sequence is a human heart
 CC mitochondrial protein of the invention.

XX SQ Sequence 364 AA;

Query Match 99.0%; Score 99; DB 7; Length 364;
 Best Local Similarity 95.0%; Pred. No. 4.2e-08;
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 PSGQAGAAASESLFISNHAY 20
 |||||:|||||:|||||
 Db 345 PSGQAGAAASESLFVSNHAY 364

RESULT 7

ADE77178
 ID ADE77178 standard; protein; 364 AA.
 XX AC ADE77178;
 XX DT 29-JAN-2004 (first entry)
 XX DE Human protein expressed in a liver disorder #87.
 XX KW human; liver disorder; hyperlipidaemia; hypertension; type II diabetes;
 KW tumour; liver; inflammatory disorder; immune response disorder;
 KW high-throughput screening; differential gene expression; gene therapy.
 XX OS Homo sapiens.
 XX FN US2003108871-A1.
 XX PD 12-JUN-2003.
 XX PF 30-JUL-2001; 2001US-00919039.
 XX PR 28-JUL-2000; 2000US-0222113P.
 XX (KASE/) KASER M R.
 XX PI Kaser MR;
 XX WPI; 2004-031227/03.
 XX N-PSDB; ADE77177.

Composition comprising several cDNAs that are differentially expressed in
 treated human C3A liver cell cultures, useful for treating liver
 disorders.

Claim 1; SEQ ID NO 343; 41pp; English.

The invention relates to a composition comprising several cDNAs that are
 differentially expressed in a liver disorder. The composition is useful
 for treating liver disorder such as hyperlipidaemia, hypertension, type
 II diabetes, tumours of the liver and disorders of the inflammatory and
 immune response. The composition is useful for a high-throughput method
 of screening several molecules or compounds to identify a ligand which
 specifically binds a cDNA. A protein encoded by the cDNA is useful for a
 high-throughput method for using a protein to screen several molecules or
 compounds to identify at least one ligand which specifically binds the
 protein which involves combining the protein encoded by the cDNA with
 several of molecules or compounds under conditions to allow specific
 binding, and detecting specific binding between the protein and a

CC molecule or compound, therefore identifying a ligand which specifically
CC binds the protein. The composition is useful for detecting and
CC quantifying differential gene expression, can be used in gene therapy, to
CC formulate prognosis and to design a treatment regimen and to monitor the
CC efficacy of treatment. The present sequence represents the amino acid
CC sequence of a protein encoded by a cDNA differentially expressed in a
CC liver disorder.
XX
SQ Sequence 364 AA;

Query Match 99.0%; Score 99; DB 8; Length 364;
Best Local Similarity 95.0%; Pred. No. 4.2e-08;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSGQAGAAASESLFVSNHAY 20
|||||:|||||:
DB 345 PSGQAGAAASESLFVSNHAY 364

RESULT 8
AD102918
ID AD102918 standard; protein; 364 AA.

AC AD102918;

DT 22-APR-2004 (first entry)

DE Human fructose-bisphosphate aldolase.

DE gene database preparation; cDNA microarray; human;

KW fructose-bisphosphate aldolase; GP2; enzyme.

XX Homo sapiens.

PN JP2004005319-A.

PD 08-JAN-2004.

PF 10-JUN-2002; 2002JP-00168894.

PR 24-APR-2002; 2002JP-00123176.

XX (KAGA-) KAGAKU GJUTSU SHINKO JIGYODAN.

PA (KOKU-) KOKURITSU SRISHIN SHINKAI CENT SOCHO.

XX WPI; 2004-113174/12.

DR N-PSDB; AD102917.

XX Gene database production method for microarray preparation, comprises
PT searching homology of a candidate sequence determined by a primer probe
PT designing unit, for a matching candidate sequence.

PS Disclosure; Fig 9; 33pp; Japanese.

XX The invention relates to a method for preparing a gene database. The
CC method comprises a search unit searching homology of a candidate sequence
CC determined by a primer probe designing unit, for determining homologous
CC presence or absence of a determined candidate sequence. The method of the
CC invention is useful for the preparation of a microarray, such as a cDNA
CC microarray. The present amino acid sequence represents a human fructose-
CC bisphosphate aldolase.
XX

SQ Sequence 364 AA;

Query Match 99.0%; Score 99; DB 8; Length 364;
Best Local Similarity 95.0%; Pred. No. 4.2e-08;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSGQAGAAASESLFVSNHAY 20
|||||:|||||:
DB 345 PSGQAGAAASESLFVSNHAY 364

RESULT 9
ADQ76754

ID ADQ76754 standard; protein; 364 AA.

AC ADQ76754;

XX 07-OCT-2004 (first entry)

DT Human fructose bisphosphate aldolase A, target for anti-HIV agent.

DE Human; fructose bisphosphate aldolase A; enzyme;

KW human immunodeficiency virus; HIV; anti-HIV; virucide.

XX Homo sapiens.

PN WO2004061088-A2.

PD 22-JUL-2004.

PF 30-DEC-2003; 2003WO-US041790.

PR 30-DEC-2002; 2002US-0436936P.

XX (PPDP-) PPD DEV LP.

PA Dunn SJ;

PI WPI; 2004-534379/51.

DR N-PSDB; ADQ76753.

XX Use of an inhibitor of a member of a biological pathway for inhibiting,
PT suppressing, treating, or preventing human immunodeficiency virus (HIV)
PT infection.

XX Claim 1; SEQ ID NO 22; 143pp; English.

XX The present sequence is that of human fructose bisphosphate aldolase A
CC (ALDOA), which has been identified as a cellular target for HIV
CC inhibition. The invention relates to methods for identifying human
CC cellular genes that encode products that are necessary for productive HIV
CC infection for use as targets in the design of therapeutic agents for
CC suppressing HIV infection. The invention also includes methods for
CC identifying biological pathways comprising the products of such cellular
CC genes, as well as substrates and metabolic products of these pathways,
CC and methods for identifying additional human cellular genes that encode
CC products comprising other members of such pathways for use as targets in
CC the design of therapeutic agents for suppressing HIV infection. It also
CC relates to methods for identifying protective compounds that inhibit HIV
CC infection and to the use of such compounds in the treatment or prevention
CC of HIV. The compounds include chemical compounds such as small molecule
CC inhibitors or substrate compounds such as products of chemical
CC combinatorial libraries, or biological compounds including peptides,
CC antisense molecules and antibodies. In one embodiment of the invention,
CC the target gene encodes a target product that is a member of the
CC glycolysis pathway of the host cell. Random fragment expression libraries
CC were constructed from mRNA isolated from HL-60 and HeLa cells, and from
CC phytohemagglutinin-stimulated peripheral blood mononuclear cells (PBMC).
CC These were used for the isolation and identification of human cell-
CC derived genetic suppressor elements (GSEs) exhibiting HIV suppressive
CC activity. The human cellular genes from which these GSEs were derived
CC were identified, and included the ALDOA gene from a PBMC library.
XX

SQ Sequence 364 AA;

Query Match 99.0%; Score 99; DB 8; Length 364;
Best Local Similarity 95.0%; Pred. No. 4.2e-08;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSGQAGAAASESLFVSNHAY 20
|||||:|||||:
DB 345 PSGQAGAAASESLFVSNHAY 364

RESULT 10
ABM81754
ID ABM81754 standard; protein; 364 AA.
XX AC ABM81754;
XX
DT 18-NOV-2004 (first entry)
XX
DE Tumour-associated antigenic target (TAT) polypeptide PRO69617, SEQ:4521.
XX
KW Tumour-associated antigenic target; TAT; human; overexpression; cancer;
KW tumour; diagnosis; cell proliferative disorder; breast cancer;
KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;
KW central nervous system cancer; bladder cancer; pancreatic cancer;
KW cervical cancer; melanoma; leukaemia; hybridisation probe;
KW chromosome identification; chromosome mapping; gene mapping;
KW gene therapy; cytostatic.
XX
OS Homo sapiens.
XX
FN WO2004030615-A2.
XX
PD 15-APR-2004.
XX
PF 29-SEP-2003; 2003WO-US028547.
XX
PR 02-OCT-2002; 2002US-0414971P.
XX
PA (GETH) GENENTECH INC.
XX
PI Wu TD, Zhang Z, Zhou Y;
XX
DR WPI; 2004-347921/32.
DR N-PSDB; ACN40010.
XX
PT New tumor-associated antigenic target polypeptides and nucleic acids,
PT useful in preparing a medicament for treating or detecting a
PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
PT prostate cancer or tumor.
XX
PS Claim 12; SEQ ID NO 4521; 7273pp; English.
XX
CC The invention relates to human tumour-associated antigenic target (TAT)
CC polypeptides, and their related nucleic acids. The TAT polypeptides are
CC overexpressed in cancer tissues compared to normal tissues, and may thus
CC serve as effective targets for the diagnosis and treatment of cancer in
CC mammals. The invention also relates to nucleic acid and polypeptide
CC sequences at least 80% identical to the TAT nucleic acids and
CC polypeptides; expression vectors and host cells comprising a TAT nucleic
CC acid; an antibody specific for a TAT polypeptide; a peptide or organic
CC molecule which binds to a TAT polypeptide; fusion proteins comprising a
CC TAT polypeptide; and methods and compositions for the treatment or
CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
CC antibodies, antagonists, binding molecules and compositions are useful
CC for diagnosing or treating a cell proliferative disorder associated with
CC increased TAT expression, particularly cancers such as breast cancer,
CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
CC cancer, pancreatic cancer, cervical cancer, cancers of the central
CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be
CC used as hybridisation probes, in chromosome and gene mapping, in
CC chromosome identification and in gene therapy. The present sequence
CC represents a TAT polypeptide of the invention
XX
SQ Sequence 364 AA;

Query Match 99.0%; Score 99; DB 8; Length 364;
Best Local Similarity 95.0%; Pred. No. 4.2e-08;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Oy 1 PSQGAGAAASESLFISNHAY 20
Dy 345 PSQGAGAAASESLFVSNHAY 364

RESULT 11
ADU46860
ID ADU46860 standard; protein; 364 AA.
XX AC ADU46860;
XX
DT 27-JAN-2005 (first entry)
XX
DE Aldolase A fructose biphosphate.
XX
KW mammal; breast; cancer; increased risk; prognosis; biomarker.
XX
OS Homo sapiens.
XX
FN WO2004097030-A2.
XX
PD 11-NOV-2004.
XX
PF 28-APR-2004; 2004WO-US013076.
XX
PR 28-APR-2003; 2003US-0466084P.
XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX (KARO-) KAROLINSKA INNOVATIONS AB.
XX
PI Bergh J, Pawitan Y, Hall P, Amler LC, Han X, Huang P, Shaw P;
XX
DR WPI; 2004-804769/79.
DR N-PSDB; ADU46827.
DR GENBANK; NP_000025.
XX
PT Identifying a mammal at increased risk for developing breast cancer by
PT correlating the level of at least one biomarker with a baseline level and
PT identifying a mammal at increased risk for developing breast cancer based
PT on the correlation.
XX
PS Claim 1; SEQ ID NO 50; 150pp; English.
XX
CC This sequence represents the aldolase A fructose biphosphate. This
CC sequence may be used in the method of the invention for identifying a
CC mammal at increased risk for developing breast cancer. The method
CC comprises correlating the level of at least one biomarker with a baseline
CC level and identifying a mammal at increased risk for developing breast
CC cancer based on the correlation. The method is useful for identifying a
CC mammal at increased risk for developing breast cancer. Preferably, it is
CC useful for prognosing breast cancer in a mammal and for identifying
CC breast cancer in a mammal, by measuring the level of a biomarker such as
CC a protein or an mRNA transcript of the biomarker.
XX
SQ Sequence 364 AA;

Query Match 99.0%; Score 99; DB 8; Length 364;
Best Local Similarity 95.0%; Pred. No. 4.2e-08;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Oy 1 PSQGAGAAASESLFISNHAY 20
Dy 345 PSQGAGAAASESLFVSNHAY 364

RESULT 12
ADX05876
ID ADX05876 standard; protein; 364 AA.
XX AC ADX05876;
XX
DT 21-APR-2005 (first entry)
XX
DE Cyclin-dependent kinase modulation biomarker SEQ ID NO 441.
XX
KW cytostatic; cyclin-dependent kinase; cdk; biomarker.
XX

(FARB) BAYER PHARM CORP.
 Taylor I, Pauloski NR, Bigwood D;
 WPI; 2005-285325/29.
 N-PSDB; ADZ70326.
 Providing a patient diagnosis for lung cancer comprises comparing the level of expression of genes or gene products in a biological sample from the patient with that from a normal individual.
 Claim 3; SEQ ID NO 12; 60pp; English.
 The invention relates to providing a patient diagnosis for lung cancer comprising comparing the level of expression of genes or gene products in a biological sample from the patient with the level of expression of genes or gene products in a biological sample from a normal individual. Also included are distinguishing between normal and disease tissues, monitoring the response of a patient being treated for lung cancer by administering an anti-cancer agent, identifying a compound useful for the treatment of lung cancer and an array for distinguishing between normal and disease tissues (comprising 2 or more probes corresponding to 2 or more genes selected from any of the 200 nucleotide sequences given in the specification, or 2 or more polypeptides comprising any of the 200 amino acid sequences given in the specification). In providing a patient diagnosis for lung cancer, one or more genes are selected from any of the 200 nucleotide sequences as mentioned in the specification, or one or more gene products are polypeptides selected from any of the 20 amino acid sequences mentioned in the specification. The methods are useful for detecting and treating lung cancer. These may also be used for designing, identifying and optimizing therapeutics for cancer. The present sequence represents a protein from one of the 200 lung cancer marker genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 Sequence 364 AA;
 Query Match 99.0%; Score 99; DB 9; Length 364;
 Best Local Similarity 95.0%; Pred. No. 4.2e-08;
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 PSQAGAGAAASESLFISNHAY 20
 |||||:|||||:|||||
 Db 345 PSQAGAGAAASESLFISNHAY 364
 RESULT 15
 ADV50900
 ID ADV50900 standard; peptide; 22 AA.
 XX ADV50900;
 AC
 XX
 DT 10-MAR-2005 (first entry)
 DE Murine brain-derived aldolase peptide 7.
 XX
 XX Beta amyloid modulator; neuroprotective; nootropic; Alzheimers disease; degeneration; neurological disease; aldolase.
 KW
 XX
 OS Mus sp.
 XX
 XX JP2004361227-A.
 XX
 XX 24-DEC-2004.
 XX
 XX 04-JUN-2003; 2003JP-00159562.
 XX
 XX 04-JUN-2003; 2003JP-00159562.
 XX
 XX (KOKU-) KOKURITSU DAIGAKU HOJIN TOHOKU DAIGAKU.
 XX

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OM protein - protein search, using sw model

Run on: February 10, 2006, 10:05:19 ; Search time 2.73063 Seconds
(without alignments)
704.723 Million cell updates/sec

Title: US-10-717-243-57

Perfect score: 100

Sequence: 1 PSQGAGAAASLSLFTSNHAY 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 80.*

1: piri.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	100.0	100.0	363	1 ADRBA	fructose-bisphosph
2	99.0	99.0	364	1 ADHUA	fructose-bisphosph
3	97.0	97.0	364	1 ADMSA	fructose-bisphosph
4	97.0	97.0	364	1 ADRTA	fructose-bisphosph
5	95.0	95.0	42	2 I51291	aldolase C - chick
6	77.0	77.0	364	2 JC4189	fructose-bisphosph
7	69.5	69.5	363	2 JC4188	fructose-bisphosph
8	68.0	68.0	364	1 ADHUC	fructose-bisphosph
9	61.0	61.0	365	2 T24514	hypothetical prote
10	60.5	60.5	363	2 I53145	zebrin II - mouse
11	59.5	59.5	337	1 ADRTC	fructose-bisphosph
12	58.0	58.0	137	2 I51292	aldolase A - chick
13	57.0	57.0	364	2 S45346	fructose-bisphosph
14	55.5	55.5	361	1 ADPP	fructose-bisphosph
15	55.5	55.5	361	2 C42263	fructose-bisphosph
16	52.0	52.0	366	2 T15951	fructose 1,6-bisph
17	50.0	50.0	364	1 ADRTB	hypothetical prote
18	48.0	48.0	179	2 AF0981	fructose-bisphosph
19	48.0	48.0	1772	2 A45532	probable exported
20	47.0	47.0	364	2 S48810	major merozoite su
21	46.0	46.0	170	2 D95178	fructose-bisphosph
22	46.0	46.0	170	2 C98045	conserved domain p
23	46.0	46.0	293	2 AE1950	hypothetical prote
24	46.0	46.0	364	1 ADHUB	cytosine-specific
25	46.0	46.0	644	2 T46277	fructose-bisphosph
26	45.0	45.0	357	1 ADSPAC	hypothetical prote
27	45.0	45.0	357	2 T12416	fructose-bisphosph
28	45.0	45.0	364	1 ADCHB	fructose-bisphosph
29	44.0	44.0	627	2 T02846	dynein light chain

RESULT 1

ADRBA

fructose-bisphosphate aldolase (EC 4.1.2.13) A - rabbit

N:Alternate names: aldolase A; fructose-1,6-bisphosphate triosephosphate-lyase A

C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 24-Apr-1984 #sequence revision 27-Nov-1985 #text change 09-Jul-2004

C:Accession: A92444; A90059; A90305; A90060; I46474; I46475; A01103

R:Tolan, D.R.; Amsden, A.B.; Putney, S.D.; Urdea, M.S.; Penhoet, E.E.

J. Biol. Chem. 259, 1127-1131, 1984

A>Title: The complete nucleotide sequence for rabbit muscle aldolase A messenger RNA.

A:Reference number: A92444; MUID:84111505; PMID:6546378

A:Accession: A92444

A:Molecule type: mRNA

A:Residues: 1-363 <TOL>

A:Cross-references: UNIPROT:P00883; UNIPARC:UPI0000125800; GB:K02300; NID:gl64751; PIDN

R:Note: Initiator Met not shown

R:Lai, C.Y.; Nakai, N.; Chang, D.

Science 183, 1204-1206, 1974

A>Title: Amino acid sequence of rabbit muscle aldolase and the structure of the active

A:Reference number: A94244; MUID:74094688; PMID:4812352

A:Contents: annotation

A:Note: the sequence reported in this paper has been revised in references A90305 and A

R:Nakai, N.; Chang, D.; Lai, C.Y.

Arch. Biochem. Biophys. 166, 347-357, 1975

A>Title: Studies on the structure of rabbit muscle aldolase. Ordering of the tryptic pe

A:Reference number: A90059; MUID:75145171; PMID:1122141

A:Accession: A90059

A:Molecule type: protein

A:Residues: 1-33,'Q',35-164 <NAK>

A:Cross-references: UNIPARC:UPI0000172P31

R:Benfield, P.A.; Forcina, B.G.; Gibbons, I.; Perham, R.N.

Biochem. J. 183, 429-444, 1979

A>Title: Extended amino acid sequences around the active-site lysine residue of class-I

A:Reference number: A90305; MUID:80109133; PMID:534504

A:Accession: A90305

A:Molecule type: protein

A:Residues: 173-200 <BEN>

A:Cross-references: UNIPARC:UPI0000172P32

R:Lai, C.Y.

Arch. Biochem. Biophys. 166, 358-369, 1975

A>Title: Studies on the structure of rabbit muscle aldolase. Determination of the prima

A:Reference number: A90060; MUID:75145172; PMID:1122142

A:Accession: A90060

A:Molecule type: protein

A:Residues: 251-272,'S',274,'E',276-277,'G',279-292,'W',294,'K',296-363 <LAI2>

A:Cross-references: UNIPARC:UPI0000172P33

R:Hartman, F.C.; Brown, J.P.

J. Biol. Chem. 251, 3057-3062, 1976

A>Title: Affinity labeling of a previously undetected essential lysyl residue in class I

A:Reference number: A92191; MUID:76190154; PMID:5453

A:Contents: annotation; active site

R:Putney, S.D.; Herlihy, W.C.; Schimmel, P.

Nature 302, 718-721, 1983
A>Title: A new troponin T and cDNA clones for 13 different muscle proteins, found by shc
A;Reference number: I46471; MUID:83167364; PMID:6687628
A;Accession: I46474
A>Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 37-55 <PUT>
A;Cross-references: UNIPARC:UPI000016C530; EMBL:V00876; NID:g1444; PIDN:CAA24245.1; PID:
A;Accession: I46475
A>Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 349-352, 'R', 354-363 <PU>
A;Cross-references: UNIPARC:UPI000016C531; EMBL:V00877; NID:g1446; PIDN:CAA24246.1; PID:
C;Comment: In vertebrates, three forms of this ubiquitous glycolytic enzyme are found, a
C;Superfamily: fructose-bisphosphate aldolase
C;Keywords: aldehyde-lyase; carbon-carbon lyase; gluconeogenesis; glycolysis; muscle; pe
F;2-363/Product: fructose-bisphosphate aldolase A #status predicted <MAT>
F;146,229,363/Active site: Lys, Lys, Tyr #status predicted

Query Match 100.0%; Score 100; DB 1; Length 363;
Best Local Similarity 100.0%; Pred. No. 1.7e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQAGAAASESLFISNHAY 20
|||||
Db 344 PSQAGAAASESLFISNHAY 363

RESULT 2
ADHUA
fructose-bisphosphate aldolase (EC 4.1.2.13) A [validated] - human
N;Alternate names: aldolase A; fructose-1,6-bisphosphate triosephosphate-lyase A
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text change 09-Jul-2004
A;Accession: S14084; A27186; S01014; S00290; S02338; A05177; S03874; S23919; I39429; I39
R;Mukai, T.; Arai, Y.; Yasui, H.; Joh, K.; Hori, K.
Eur. J. Biochem. 195, 781-787, 1991
A>Title: An additional promoter functions in the human aldolase A gene, but not in rat.
A;Reference number: S14084; MUID:91153319; PMID:1999195
A;Accession: S14084
A;Molecule type: DNA
A;Residues: 1-364 <MK>
A;Cross-references: UNIPROT:P04075; UNIPARC:UPI00000000C5D
Rizzo, P.; Costanzo, P.; Lupo, A.; Rippa, E.; Borghese, A.M.; Paolella, G.; Salvatore,
Eur. J. Biochem. 164, 9-13, 1987
A>Title: A new human species of aldolase A mRNA from fibroblasts.
A;Reference number: A27186; MUID:87161904; PMID:3030757
A;Accession: A27186
A;Molecule type: mRNA
A;Residues: 1-72, 'G', 74-195, 'A', 197-229, 'N', 231-279, 'S', 281-364 <IZ2>
A;Cross-references: UNIPARC:UPI00000000C5D; GB:X05236; NID:g28596; PIDN:CAA28861.1; PID:9
A;Experimental source: fibroblast
Rizzo, P.; Costanzo, P.; Lupo, A.; Rippa, E.; Paolella, G.; Salvatore, F.
Eur. J. Biochem. 174, 569-578, 1988
A>Title: Human aldolase A gene. Structural organization and tissue-specific expression b
A;Reference number: S01014; MUID:88271327; PMID:3391172
A;Accession: S01014
A;Molecule type: DNA
A;Residues: 1-72, 'G', 74-195, 'A', 197-229, 'N', 231-279, 'S', 281-364 <IZ2>
A;Cross-references: UNIPARC:UPI000016A52D; GB:X12447; NID:g28613; PIDN:CAA30979.1; PID:9
R;Fremont, P.S.; Dunbar, B.; Fothergill-Gilmore, L.A.
Biochem. J. 249, 779-788, 1988
A>Title: The complete amino acid sequence of human skeletal-muscle fructose-bisphosphate
A;Reference number: S00290; MUID:88183272; PMID:3355497
A;Accession: S00290
A;Molecule type: protein
A;Residues: 2-358, 'I', 360-364 <FRE>
A;Cross-references: UNIPARC:UPI0000172F2C
R;Maire, P.; Gautron, S.; Hakim, V.; Gregori, C.; Mennecier, F.; Kahn, A.
J. Mol. Biol. 197, 425-438, 1987
A>Title: Characterization of three optional promoters in the 5' region of the human aldo
A;Reference number: S02338; MUID:88155643; PMID:3441006
A;Accession: S02338

A;Molecule type: DNA
A;Residues: 1-108 <MAI>
A;Cross-references: UNIPARC:UPI000016A521; EMBL:X06352; NID:g28594; PIDN:CAA29654.1; PID:
R;Fremont, P.S.; Dunbar, B.; Fothergill, L.A.
Arch. Biochem. Biophys. 228, 342-352, 1984
A>Title: Human skeletal-muscle aldolase: N-terminal sequence analysis of CNBr- and o-iod
A;Reference number: A05177; MUID:84126818; PMID:6696436
A;Accession: A05177
A;Molecule type: protein
A;Residues: 2-63;148-358 <FR2>
A;Cross-references: UNIPARC:UPI0000172F2D; UNIPARC:UPI0000172F2E
R;Sakakibara, M.; Takahashi, I.; Takasaki, Y.; Mukai, T.; Hori, K.
Biochim. Biophys. Acta 1007, 334-342, 1989
A>Title: Construction and expression of human aldolase A and B expression plasmids in Es
A;Reference number: S03874; MUID:89194215; PMID:2649152
A;Accession: S03874
A;Molecule type: mRNA
A;Residues: 1-33;357-364 <SAK>
A;Cross-references: UNIPARC:UPI0000172F2F; UNIPARC:UPI0000172F30
R;Lee, K.N.; Maxwell, M.D.; Patterson Jr., M.K.; Birckbichler, P.J.; Conway, E.
Biochim. Biophys. Acta 1136, 12-16, 1992
A>Title: Identification of transglutaminase substrates in HT29 colon cancer cells: use o
A;Reference number: S23919; MUID:92353128; PMID:1353685
A;Accession: S23919
A;Molecule type: protein
A;Residues: 2-16 <LEE>
A;Cross-references: UNIPARC:UPI0000071F95
R;Gamblin, S.J.; Davies, G.J.; Grimes, J.M.; Jackson, R.M.; Littlechild, J.A.; Watson, H.
J. Mol. Biol. 219, 573-576, 1991
A>Title: Activity and Specificity of Human Aldolases.
A;Reference number: A43787; MUID:91278081; PMID:2056525
A;Contents: annotation; active site
R;Sakakibara, M.; Mukai, T.; Hori, K.
Biochem. Biophys. Res. Commun. 131, 413-420, 1985
A>Title: Nucleotide sequence of a cDNA clone for human aldolase: a messenger RNA in the
A;Reference number: I39429; MUID:85306986; PMID:3840020
A;Accession: I39429
A>Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-364 <RES>
A;Cross-references: UNIPARC:UPI00000000C5D; GB:M11560; NID:g178350; PIDN:AAAS1690.1; PID:
R;Tolan, D.R.; Niclas, J.; Bruce, B.D.; Lebo, R.V.
Am. J. Hum. Genet. 41, 907-924, 1987
A>Title: Evolutionary implications of the human aldolase-A, -B, -C, and -pseudogene chr
A;Reference number: I39435; MUID:88046782; PMID:3674018
A;Accession: I39435
A;Molecule type: mRNA
A;Residues: 139-364 <TOL>
A;Cross-references: UNIPARC:UPI000016A52E; GB:M21190; NID:g178403; PIDN:AAAS1697.1; PID:
C;Comment: In vertebrates, three forms of this ubiquitous glycolytic enzyme are found, f
C;Genetics:
A;Gene: GDB:ALDOA
A;Cross-references: GDB:118993; OMIM:103850
A;Map position: 16q22.2-16q22.2
A;Introns: 38/1
C;Superfamily: fructose-bisphosphate aldolase
C;Keywords: aldehyde-lyase; carbon-carbon lyase; gluconeogenesis; glycolysis; muscle; p
F;2-364/Product: fructose-bisphosphate aldolase A #status experimental <MAT>
F;147,230,364/Active site: Lys, Lys, Tyr #status experimental

Query Match 99.0%; Score 99; DB 1; Length 364;
Best Local Similarity 95.0%; Pred. No. 2.4e-08;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQAGAAASESLFISNHAY 20
|||||
Db 345 PSQAGAAASESLFISNHAY 364

RESULT 3
ADMSA
fructose-bisphosphate aldolase (EC 4.1.2.13) A - mouse
N;Alternate names: aldolase A; fructose-1,6-bisphosphate triosephosphate-lyase A

C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C:Accession: S06323; B25388; A37062
R:Mestek, A.; Stauffer, J.; Tolan, D.R.; Ciejek-Baez, E.
Nucleic Acids Res. 15, 10595, 1987
A:Title: Sequence of a mouse brain aldolase A cDNA.
A:Reference number: S06323; MUID:88096598; PMID:3697100
A:Accession: S06323
A:Molecule type: mRNA
A:Residues: 1-364 <MES>
A:Cross-references: UNIPARC:U01000016CBFC; GB:Y00516; NID:949914; PIDN:Q
R:Paolella, G.; Buono, P.; Mancini, P.P.; Izzo, P.; Salvatore, P.
Eur. J. Biochem. 156, 229-235, 1986
A:Title: Structure and expression of mouse aldolase genes. Brain-specific aldolase A c
A:Reference number: A91165; MUID:86192445; PMID:3009179
A:Accession: B25388
A:Molecule type: mRNA
A:Residues: 99-280, 'C', 282-355 <PAO>
A:Cross-references: UNIPARC:U010000172F34; UNIPARC:U01000172F35; GB:J05517
A:Experimental source: strain RIII S/J
R:Stauffer, J.K.; Colbert, M.C.; Ciejek-Baez, E.
J. Biol. Chem. 265, 11773-11782, 1990
A:Title: Nonconservative utilization of aldolase A alternative promoters.
A:Reference number: A37062; MUID:90307699; PMID:2365699
A:Accession: A37062
A:Molecule type: DNA
A:Residues: 1-266; 295-364 <STA>
A:Cross-references: UNIPARC:U01000172F34; UNIPARC:U01000172F35; GB:J05517
A:Experimental source: strain RIII S/J
C:Superfamily: fructose-bisphosphate aldolase
C:Keywords: aldehyde-lyase; carbon-carbon lyase; gluconeogenesis; glycolysis; muscle; pe
F:2-364/Product: fructose-bisphosphate aldolase A #status predicted <MAY>
F:147,230,364/Active site: Lys, Lys, Tyr #status predicted

Query Match 97.0%; Score 97; DB 1; Length 364;
Best Local Similarity 95.0%; Pred. No. 5.2e-08;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQGAGAAASLSLFTSNHAY 20
|||||
DB 345 PSQGAGAAASLSLFTSNHAY 364

RESULT 4
ADRTA
fructose-bisphosphate aldolase (EC 4.1.2.13) A - rat
N:Alternate names: aldolase A; fructose-1,6-bisphosphate triosephosphate-lyase A
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 31-Dec-2004
C:Accession: A24532; A25383; I53307; I56408
R:Joh, K.; Mukai, T.; Yatsuki, H.; Hori, K.
Gene 39, 17-24, 1985
A:Title: Rat aldolase A messenger RNA: the nucleotide sequence and multiple mRNA species
A:Reference number: A24532; MUID:86083188; PMID:2416636
A:Accession: A24532
A:Molecule type: mRNA
A:Residues: 1-364 <JOH>
A:Cross-references: UNIPROT:P05065; UNIPROT:Q63038; UNIPARC:U01000170873; GB:M14420; NI
R:Mukai, T.; Joh, K.; Arai, Y.; Yatsuki, H.; Hori, K.
J. Biol. Chem. 261, 3347-3354, 1986
A:Title: Tissue-specific expression of rat aldolase A mRNAs: three molecular species dif
A:Reference number: A25383; MUID:86140113; PMID:3753397
A:Accession: A25383
A:Molecule type: mRNA
A:Residues: 1-144, 'P', 146-164, 'M', 166-364 <MUK>
A:Cross-references: UNIPARC:U01000167983; GB:M12919; NID:9202834; PIDN:AAA40714.1; PID:
R:Tautsami, R.; Tautsami, K.
Eur. J. Biochem. 142, 161-164, 1984
A:Title: Two different aldolase A mRNA species in rat tissues.
A:Reference number: I53307; MUID:84261525; PMID:6086339
A:Accession: I53307
A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA
A:Residues: 324-329, 'Q', 331-356 <RES>
A:Cross-references: UNIPARC:U010000E7075; GB:M28282; NID:9202849; PIDN:AAA40720.1; PID:
R:Joh, K.; Arai, Y.; Mukai, T.; Hori, K.
J. Mol. Biol. 190, 401-410, 1986
A:Title: Expression of three mRNA species from a single rat aldolase A gene, differing i
A:Reference number: I56408; MUID:87060996; PMID:3783705
A:Accession: I56408
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-108 <RE2>
A:Cross-references: UNIPARC:U010000172F36; EMBL:X04261; NID:955639; PIDN:CAA27815.1; PI:
C:Genetics:
A:Introns: 38/1
C:Keywords: aldehyde-lyase; carbon-carbon lyase; gluconeogenesis; glycolysis; muscle; p
F:2-364/Product: fructose-bisphosphate aldolase A #status predicted <MAY>
F:147,230,364/Active site: Lys, Lys, Tyr #status predicted

Query Match 97.0%; Score 97; DB 1; Length 364;
Best Local Similarity 95.0%; Pred. No. 5.2e-08;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQGAGAAASLSLFTSNHAY 20
|||||
DB 345 PSQGAGAAASLSLFTSNHAY 364

RESULT 5
I51291
aldolase C - chicken (fragment)
C:Species: Gallus gallus (chicken)
C:Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 09-Jul-2004
C:Accession: I51291
R:Meighan-Mantha, R.L.; Tolan, D.R.
J. Cell. Biochem. 57, 423-431, 1995
A:Title: Noncoordinate changes in the steady-state mRNA expressed from aldolase A and
A:Reference number: I51291; MUID:95286677; PMID:7768978
A:Accession: I51291
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-42 <MEI>
A:Cross-references: UNIPROT:Q92007; UNIPARC:U0100000FDF44; GB:S78288; NID:9999389; PIDN:
C:Superfamily: fructose-bisphosphate aldolase

Query Match 95.0%; Score 95; DB 2; Length 42;
Best Local Similarity 95.0%; Pred. No. 1e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PSQGAGAAASLSLFTSNHAY 20
|||||
DB 23 PSQGAGAAASLSLFTSNHAY 42

RESULT 6
JC4189
fructose-bisphosphate aldolase (EC 4.1.2.13), non-muscle-type - Pacific lamprey
N:Alternate names: non-muscle-type aldolase
C:Species: Lampetra tridentata, Entosphenus tridentatus (Pacific lamprey)
C:Date: 27-Sep-1995 #sequence_revision 27-Oct-1995 #text_change 20-Jun-2000
C:Accession: JC4189
R:Zhang, R.; Yatsuki, H.; Kusakabe, T.; Iwabe, N.; Miyata, T.; Imai, T.; Yoshida, M.; H
J. Biochem. 117, 545-553, 1995
A:Title: Structures of cDNAs encoding the muscle-type and non-muscle-type isozymes of la
A:Reference number: JC4188; MUID:95355304; PMID:7629020
A:Accession: JC4189
A:Molecule type: mRNA
A:Residues: 1-364 <ZHA>
A:Cross-references: UNIPARC:U010001257F9; DBJ:D38619; NID:91619826; PIDN:BA07607.1; P
C:Comment: This is a glycolytic enzyme that catalyzes the reversible cleavage of fructos
C:Superfamily: fructose-bisphosphate aldolase
C:Keywords: aldehyde-lyase; carbon-carbon lyase; muscle
F:230/Active site: Lys #status predicted

Query Match 77.0%; Score 77; DB 2; Length 364;
 Best Local Similarity 70.0%; Pred. No. 9.4e-05; Mismatches 2; Indels 0; Gaps 0;
 Matches 14; Conservative 4;

QY 1 PSQAGAAASESLFISNHAY 20
 ||:|||||:|||||
 DB 345 PAGSGSAAASESLFIANHAY 364

RESULT 7
 JC4188
 fructose-bisphosphate aldolase (EC 4.1.2.13), muscle-type - Pacific lamprey
 N:Alternate names: muscle-type aldolase
 C:Species: Lampetra tridentata, Entosphenus tridentatus (Pacific lamprey)
 C:Date: 27-Sep-1995 #sequence_revision 27-Oct-1995 #text_change 20-Jun-2000
 C:Accession: JC4188
 R:Zhang, R.; Yatsuki, H.; Kusakabe, T.; Iwabe, N.; Miyata, T.; Yoshida, M.; Horiuchi, J. Biochem. 117, 545-553, 1995
 A:Title: Structures of cDNAs encoding the muscle-type and non-muscle-type isozymes of lampetra tridentata
 A:Reference number: JC4188; MUID:95355304; PMID:7629020
 A:Accession: JC4188
 A:Molecule type: mRNA
 A:Residues: 1-363 <ZHA>
 A:Cross-references: UNIPARC:UPI00001257EP; DDBJ:D38620; NID:G1619827; PIDN:BAA07608.1; EMBL:D38620
 C:Comment: This is a glycolytic enzyme that catalyzes the reversible cleavage of fructose-1,6-bisphosphate into fructose-6-phosphate and dihydroxyacetone phosphate
 C:Superfamily: fructose-bisphosphate aldolase
 C:Keywords: aldehyde-lyase; carbon-carbon lyase; muscle
 F:230/Active site: Lys #status predicted

Query Match 69.5%; Score 69.5; DB 2; Length 363;
 Best Local Similarity 70.0%; Pred. No. 0.0016; Mismatches 2; Indels 1; Gaps 1;
 Matches 14; Conservative 3;

QY 1 PSQAGAAASESLFISNHAY 20
 ||:|||||:|||||
 DB 345 PTG-TGAAGESLFVANHY 363

RESULT 8
 ADHUC
 fructose-bisphosphate aldolase (EC 4.1.2.13) C - human
 N:Alternate names: aldolase C; fructose-1,6-bisphosphate triosephosphate-lyase C
 C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
 C:Accession: A25861; S00863; S13192
 R:Kottmann, W.H.; Deselms, K.R.; Niclas, J.; Camerato, T.; Holman, P.S.; Green, C.J.; Tschopp, A. Biochem. 137, 145, 1987
 A:Title: The complete amino acid sequence of the human aldolase C isozyme derived from 9L cells
 A:Reference number: A25861; MUID:87185595; PMID:3105602
 A:Accession: A25861
 A:Molecule type: DNA
 A:Residues: 1-364 <ROT>
 A:Cross-references: UNIPROT:P09972; UNIPARC:UPI0000000C53; GB:X05196; NID:G28598; PIDN:Q05196
 R:Buono, P.; Paoletti, G.; Mancini, P.P.; Izzo, P.; Salvatore, F.
 Nucleic Acids Res. 16, 4733, 1988
 A:Title: The complete nucleotide sequence of the gene coding for the human aldolase C.
 A:Reference number: S00863; MUID:88247784; PMID:3267224
 A:Accession: S00863
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-310, 'V', 312-364 <BUO1>
 A:Cross-references: UNIPARC:UPI000016A523; GB:X07292; NID:G28600; PIDN:CAA30270.1; PID:G28600
 R:Buono, P.; Mancini, P.P.; Izzo, P.; Salvatore, F.
 Eur. J. Biochem. 192, 805-811, 1990
 A:Title: Characterization of the transcription-initiation site and of the promoter region of the human aldolase C gene
 A:Reference number: S13192; MUID:91006178; PMID:2209624
 A:Accession: S13192
 A:Molecule type: DNA
 A:Residues: 1-310, 'V', 312-364 <BUO2>
 A:Cross-references: UNIPARC:UPI000016A523; GB:X07292; NID:G28600; PIDN:CAA30270.1; PID:G28600
 C:Genetics:
 A:Gene: GDB:ALDOC
 A:Cross-references: GDB:119670; OMIM:103870

A:Map position: 17pter-17qter
 A:Introns: 38/1; 108/3; 127/1; 180/3; 208/3; 267/1; 333/3
 C:Superfamily: fructose-bisphosphate aldolase
 C:Keywords: aldehyde-lyase; brain; carbon-carbon lyase; gluconeogenesis; glycolysis; penicillin resistance
 F:2-364/Product: fructose-bisphosphate aldolase C #status predicted <MAT>
 F:147,230,364/Active site: Lys, Lys, Tyr #status predicted

Query Match 68.0%; Score 68; DB 1; Length 364;
 Best Local Similarity 63.2%; Pred. No. 0.0028; Mismatches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 SGOAGAAASESLFISNHAY 20
 ||:|||||:|||||
 DB 346 SGEDGAAASQSLFIANHAY 364

RESULT 9
 T24514
 hypothetical protein T05D4.1 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T24514
 R:McMurray, A.
 submitted to the EMBL Data Library, October 1996
 A:Reference number: Z19902
 A:Accession: T24514
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-365 <WIL>
 A:Cross-references: UNIPROT:P54216; UNIPARC:UPI0000164172; EMBL:Z81115; PIDN:CAB03291.1; EMBL:Z81115
 A:Experimental source: clone T05D4
 C:Genetics:
 A:Gene: CESP:T05D4.1
 A:Map position: 3
 A:Introns: 32/1; 190/3
 C:Superfamily: fructose-bisphosphate aldolase

Query Match 61.0%; Score 61; DB 2; Length 365;
 Best Local Similarity 68.8%; Pred. No. 0.038; Mismatches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 5 AGAAASESLFISNHAY 20
 ||:|||||:|||||
 DB 350 ADAAAASQSLFVANHY 365

RESULT 10
 I53145
 zebrin II - mouse
 C:Species: Mus sp. (mouse)
 C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 22-Jun-1999
 C:Accession: I53145
 R:Ahn, A.H.; Dziennis, S.; Hawkes, R.; Herrup, K.
 Development 120, 2081-2090, 1994
 A:Title: The cloning of zebrin II reveals its identity with aldolase C.
 A:Reference number: I53145; MUID:95009537; PMID:7925012
 A:Accession: I53145
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: mRNA
 A:Residues: 1-363 <RES>
 A:Cross-references: UNIPARC:UPI00000E5AF7; GB:S72537; NID:G619372; PIDN:AAB32064.1; PID:G619372
 C:Superfamily: fructose-bisphosphate aldolase

Query Match 60.5%; Score 60.5; DB 2; Length 363;
 Best Local Similarity 68.4%; Pred. No. 0.046; Mismatches 13; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY 2 SGOAGAAASESLFISNHAY 20
 ||:|||||:|||||
 DB 346 SGEDGAAASQSLFIANHAY 363

RESULT 11

Db 119 SGDSGAGQCSLYVANHAY 137

RESULT 13
S45346
fructose-bisphosphate aldolase [EC 4.1.2.13] C, brain-type - African clawed frog
N/Alternate names: aldolase C
C/Species: Xenopus laevis (African clawed frog)
C/Date: 16-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 09-Jul-2004
C/Accession: S45346; I51247
R;Atsuchi, Y.; Yamana, K.; Yatsuki, H.; Hori, K.; Ueda, S.; Shiokawa, K.
Biochim. Biophys. Acta 1218, 153-157, 1994
A;Title: Cloning of a brain-type aldolase cDNA and changes in its mRNA level during oogenesis
A;Reference number: I51247; MUID:94289472; PMID:8018714
A;Accession: S45346
A;Molecule type: mRNA
A;Residues: 1-364 <ATS>
A;Cross-references: UNIPROT:Q91384; UNIPARC:UPI00000PBC29; GB:S73606; NID:G688323; PIDN
A;Experimental source: brain
A;Note: translation of initiator Met is not shown
C;Genetics:
A;Gene: XALD3
C;Superfamily: fructose-bisphosphate aldolase
C;Keywords: aldehyde-lyase; carbon-carbon lyase
F;2-364/Product: fructose-bisphosphate aldolase C #status predicted <MAT>

Query Match 57.0%; Score 57; DB 2; Length 364;
Best Local Similarity 47.4%; Pred. No. 0.17;
Matches 9; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 2 SQGAGAAASESLFISNHAY 20
||| :|:|:|:|
346 SGDSGAGQCSLYVANHAY 364

Db 346 SGDSGAGQCSLYVANHAY 364

RESULT 14
ADRF
fructose-bisphosphate aldolase [EC 4.1.2.13] - fruit fly (Drosophila melanogaster)
C/Species: Drosophila melanogaster
C/Date: 30-Sep-1991 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
C/Accession: B42027; S06439; A28855; S22186
R;Kim, J.; Yim, J.J.; Wang, S.; Dorsett, D.
Mol. Cell. Biol. 12, 773-783, 1992
A;Title: Alternate use of divergent forms of an ancient exon in the fructose-1,6-bisphosphatase
A;Reference number: A42027; MUID:92123202; PMID:1732743
A;Accession: B42027
A;Molecule type: DNA
A;Residues: 1-361 <KIM>
A;Cross-references: UNIPROT:P07764; UNIPARC:UPI000016BACB; EMBL:X60064; NID:G7571; PIDN
A;Note: sequence extracted from NCBI backbone (NCBI:76564, NCBI:P:87828)
R;Malek, A.A.; Hy, M.; Honegger, A.; Rose, K.; Brenner-Holzach, O.
Arch. Biochem. Biophys. 266, 10-31, 1988
A;Title: Fructose-1,6-bisphosphate aldolase from Drosophila melanogaster: primary structure
A;Reference number: S06439; MUID:89024658; PMID:3140728
A;Accession: S06439
A;Molecule type: protein
A;Residues: 2-110,'K',112-200,'R',202-250,'A',252-361 <NAL>
A;Cross-references: UNIPARC:UPI0000125817
R;Brenner-Holzach, O.; Zumsteg, C.
Arch. Biochem. Biophys. 214, 89-101, 1982
A;Title: Fructose 1,6-bisphosphate aldolase of Drosophila melanogaster: comparative sequencing
A;Reference number: A28855; MUID:82205133; PMID:6805442
A;Accession: A28855
A;Molecule type: protein
A;Residues: 170-179,'QS',182-200,'R',202-224,'Q',226-250,'A',252-272 <BRE>
A;Cross-references: UNIPARC:UPI0000172F3D
A;Note: peptides were ordered by homology with the rabbit sequence
C;Genetics:
A;Gene: FlyBase:Ald
A;Cross-references: FlyBase:FBgn0000064
C;Superfamily: fructose-bisphosphate aldolase
C;Keywords: aldehyde-lyase; carbon-carbon lyase; gluconeogenesis; glycolysis; pentose
F;2-361/Product: fructose-bisphosphate aldolase #status experimental <MAT>

F:147,230,361/Active site: Lys, Lys, Tyr #status predicted

Query Match 55.5%; Score 55.5; DB 1; Length 361;
Best Local Similarity 63.2%; Pred. No. 0.3;
Matches 12; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 2 SQQAGAAASESLFISNHAY 20
: ||| | ||| : |||
Db 344 AGSAG-AGSGSLFVANHAY 361

RESULT 15

C42263
fructose 1,6-bisphosphate aldolase - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: C42263
R:Shaw-Lee, R.; Lissemore, J.L.; Sullivan, D.T.; Tolan, D.R.
J. Biol. Chem. 267, 3959-3967, 1992
A:Title: Alternative splicing of fructose 1,6-bisphosphate aldolase transcripts in Drosophila
A:Reference number: A42263; MUID:92156139; PMID:1740444
A:Accession: C42263
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-361 <SHA>
A:Cross-references: UNIPROT:P07764; UNIPARC:UPI00001248A2; GB:M98351; GB:M76409; NID:gl5
A:Note: sequence extracted from NCBI backbone (NCBI:82659, NCBIP:93286)
C:Genetics:
A:Gene: FlyBase:Ald
A:Cross-references: FlyBase:FBgn0000064
C:Superfamily: fructose-bisphosphate aldolase

Query Match 55.5%; Score 55.5; DB 2; Length 361;
Best Local Similarity 63.2%; Pred. No. 0.3;
Matches 12; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 2 SQQAGAAASESLFISNHAY 20
: ||| | ||| : |||
Db 344 AGSAG-AGSGSLFVANHAY 361

Search completed: February 10, 2006, 10:14:05
Job time : 3.73063 secs

GenCore version 5.1.7

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OM protein - protein search, using sw model

Run on: February 10, 2006, 10:00:34 ; Search time 16.9004 Seconds
(without alignments)
834.927 Million cell updates/sec

Title: US-10-717-243-57

Perfect score: 100

Sequence: 1 PSQQAARSLFISFNHAY 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	100	100.0	363	1 ALDOA RABIT	P00883 oryctolagus
2	99	99.0	260	2 Q9BWD9 HUMAN	Q9BWD9 homo sapien
3	99	99.0	363	1 ALDOA HUMAN	P04075 homo sapien
4	99	99.0	364	2 Q6F110 HUMAN	Q6F110 homo sapien
5	99	99.0	364	2 Q5NVR5 POMPY	Q5NVR5 pongo pygma
6	97	97.0	363	1 ALDOA MOUSE	P05064 mus musculus
7	97	97.0	363	1 ALDOA RAT	P05065 rattus norv
8	97	97.0	364	2 Q5FWB7 MOUSE	Q5FWB7 mus musculus
9	97	97.0	364	2 Q6NY00 MOUSE	Q6NY00 mus musculus
10	95	95.0	42	2 Q92007 CHICK	Q92007 gallus gall
11	94	94.0	276	2 Q4P523 MACFA	Q4P523 macaca fasc
12	94	94.0	704	2 Q8WNT7 MACFA	Q8WNT7 macaca fasc
13	89	89.0	331	2 Q9CFQ9 MOUSE	Q9CFQ9 ambystoma m
14	88	88.0	364	2 Q9CRC1 MOUSE	Q9CRC1 mus muscu
15	88	88.0	364	2 Q6GL64 XENTR	Q6GL64 xenopus tro
16	85	85.0	364	2 Q6AY07 RAT	Q6AY07 rattus norv
17	83	83.0	364	2 Q12975 XENLA	Q12975 xenopus lae
18	83	83.0	364	2 Q76BE7 AMICA	Q76BE7 amia calva
19	82	82.0	331	2 Q7SYU5 XENLA	Q7SYU5 xenopus lae
20	79	79.0	279	2 Q76BF4 LEPOS	Q76BF4 lepisosteus
21	79	79.0	331	2 Q5XGT3 XENLA	Q5XGT3 xenopus lae
22	79	79.0	364	1 Q76BD9 ACIBE	Q76BD9 lampetra ja
23	77	77.0	364	1 Q76BD9 ACIBE	Q76BD9 lampetra ja
24	76	76.0	331	2 Q76BI2 PROAN	Q76BI2 protopetere
25	75	75.0	364	2 Q8JH72 BRARE	Q8JH72 brachydanio
26	75	75.0	364	2 Q803Q7 BRARE	Q803Q7 brachydanio
27	74	74.0	331	2 Q76BB1 9CHON	Q76BB1 callorhinch
28	73	73.0	331	2 Q76BC5 9CHON	Q76BC5 cephaloscyll
29	72	72.0	331	2 Q76BD2 POLOR	Q76BD2 polypteru
30	72	72.0	364	2 Q76BD9 ACIBE	Q76BD9 brachydanio
31	71	71.0	331	2 Q76BD9 ACIBE	Q76BD9 acipenser b

32	71	71.0	331	2 Q9USF9 EPTBU	Q9USF9 eptatretus
33	70	70.0	331	2 Q76BE0 ACIBE	Q76BE0 acipenser b
34	69.5	69.5	363	1 ALP1 LAMJA	P53445 lampetra ja
35	69	69.0	331	2 Q76BB8 9CHON	Q76BB8 brachydanio
36	69	69.0	364	2 Q7ZW73 BRARE	Q7ZW73 brachydanio
37	68	68.0	363	1 ALDOC HUMAN	P09972 homo sapien
38	68	68.0	363	1 ALDOC MACFA	Q9GKW3 macaca fasc
39	68	68.0	363	1 ALDOC PANTR	Q5R1X4 pan troglod
40	68	68.0	364	2 Q6FH94 HUMAN	Q6FH94 homo sapien
41	68	68.0	364	2 Q4R4S9 MACFA	Q4R4S9 macaca fasc
42	68	68.0	394	2 Q6P0L5 HUMAN	Q6P0L5 homo sapien
43	65	65.0	331	2 Q76BC3 9CHON	Q76BC3 cephaloscyll
44	64	64.0	40	2 Q6UV41 PIG	Q6UV41 sus scrofa
45	64	64.0	330	2 Q76BF9 ORYLA	Q76BF9 oryzias lat

ALIGNMENTS

RESULT 1

ID ALDOA RABIT STANDARD; PRT; 363 AA.
AC P00883; Q28671;
DT 21-JUL-1986 (Rel. 01, Created)
DE Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Muscle-type aldolase).
GN Name=ALDOA;
OS Oryctolagus cuniculus (Rabbit);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=74094688; PubMed=4812352;
RA Lai C.-Y., Nakai N., Chang D.;
RT "Amino acid sequence of rabbit muscle aldolase and the structure of the active center."
RL Science 183:1204-1206(1974).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=84111505; PubMed=6546378;
RA Tolan D.R., Amsden A.B., Putney S.D., Urdea M.S., Penhoet E.B.;
RT "The complete nucleotide sequence for rabbit muscle aldolase A messenger RNA."
RL J. Biol. Chem. 259:1127-1131(1984).
RN [3]
RP PROTEIN SEQUENCE OF 1-164.
RX MEDLINE=75145171; PubMed=1122141;
RA Nakai N., Chang D., Lai C.-Y.;
RT "Studies on the structure of rabbit muscle aldolase. Ordering of the tryptic peptides; sequence of 164 amino acid residues in the NH2-terminal BRN peptide."
RL Arch. Biochem. Biophys. 166:347-357(1975).
RN [4]
RP PROTEIN SEQUENCE OF 173-200, AND SEQUENCE REVISION.
RX MEDLINE=80109133; PubMed=534504;
RA Benfield P.A., Forcina B.G., Gibbons I., Perham R.N.;
RT "Extended amino acid sequences around the active-site lysine residue of class-I fructose 1,6-bisphosphate aldolases from rabbit muscle, sturgeon muscle, trout muscle and ox liver."
RL Biochem. J. 183:429-444(1979).
RN [5]
RP PROTEIN SEQUENCE OF 251-363, AND SEQUENCE REVISION.
RX MEDLINE=75145172; PubMed=1122142;
RA Lai C.-Y.;
RT "Studies on the structure of rabbit muscle aldolase. Determination of the primary structure of the COOH-terminal BRN peptide; the complete sequence of the subunit polypeptide chain."
RL Arch. Biochem. Biophys. 166:358-368(1975).
RN [6]
RP NUCLEOTIDE SEQUENCE OF 37-55 AND 349-363.

RX MEDLINE=83167564; PubMed=6687628;
 RA Putney S.D., Herlihy W.C., Schimmel P.R.;
 RT "A new troponin T and cDNA clones for 13 different muscle proteins,
 found by shotgun sequencing.";
 RL Nature 302:718-721(1983).
 RN [7]
 RP ACTIVE SITE.
 RX MEDLINE=74163196; PubMed=4857186;
 RA Hartman F.C., Welch M.H.;
 RT "Identification of the histidyl residue of rabbit muscle aldolase
 alkylated by N-bromosuccinylmethanolamine phosphate.";
 RL Biochem. Biophys. Res. Commun. 57:85-92(1974).
 RN [8]
 RP ACTIVE SITE.
 RX MEDLINE=76190154; PubMed=5453;
 RA Hartman F.C., Brown J.P.;
 RT "Affinity labeling of a previously undetected essential lysyl residue
 in class I fructose biphosphate aldolase.";
 RL J. Biol. Chem. 251:3057-3062(1976).
 RN [9]
 RP SUBSTRATE-BINDING SITE.
 RX MEDLINE=80046697; PubMed=499203;
 RA Patthy L., Varadi A., Thesz J., Kovacs K.;
 RT "Identification of the C-1-phosphate-binding arginine residue of
 rabbit-muscle aldolase. Isolation of 1,2-cyclohexanedione-labeled
 peptide by chemisorption chromatography.";
 RL Eur. J. Biochem. 99:309-313(1979).
 RN [10]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE=97143309; PubMed=8989320;
 RA Blom N., Sygusch J.;
 RT "Product binding and role of the C-terminal region in class I D-
 fructose 1,6-bisphosphate aldolase.";
 RL Nat. Struct. Biol. 4:36-39(1997).
 RN [11]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 2-344 IN COMPLEX WITH
 SUBSTRATE, AND MUTAGENESIS OF GLU-34; ARG-42; LYS-146 AND ARG-303.
 RX MEDLINE=99435739; PubMed=10504235; DOI=10.1021/bi9828371;
 RA Choi K.H., Mazurkiewicz A.S., Morris A.J., Ucheza D., Tolan D.R.,
 Allen K.N.;
 RT "Structure of a fructose-1,6-bisphosphate aldolase liganded to its
 natural substrate in a cleavage-defective mutant at 2.3 A.";
 RL Biochemistry 38:12655-12664(1999).
 RN [12]
 RP X-RAY CRYSTALLOGRAPHY (2.46 ANGSTROMS), AND MUTAGENESIS OF GLU-187;
 GLU-189 AND LYS-229.
 RX MEDLINE=21883945; PubMed=11779856; DOI=10.1074/jbc.M107600200;
 RA Maurady A., Zdanov A., de Moissac D., Beaudry D., Sygusch J.;
 RT "A conserved glutamate residue exhibits multifunctional catalytic
 roles in D-fructose-1,6-bisphosphate aldolases.";
 RL J. Biol. Chem. 277:9474-9483(2002).
 CC -/- CATALYTIC ACTIVITY: D-fructose 1,6-bisphosphate = glycerone
 phosphate + D-glyceraldehyde 3-phosphate.
 CC -/- PATHWAY: Glycolysis; sixth step.
 CC -/- SUBUNIT: Tetramer of nearly identical chains, alpha and beta,
 which differ at only 1 position.
 CC -/- PTM: Asn-360 in the alpha chain is deaminated in the beta chain.
 CC -/- MISCELLANEOUS: In vertebrates, three forms of this ubiquitous
 glycolytic enzyme are found, aldolase A in muscle, aldolase B in
 liver and aldolase C in brain.
 CC -/- SIMILARITY: Belongs to the class I fructose-bisphosphate aldolase
 family.
 CC -/- DATABASE: NAME=Worthington enzyme manual;
 WWW="http://www.worthington-biochem.com/ALD/".
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use as long as its content is in no way modified and this statement is not
 removed.
 CC -----
 DR EMBL; K02300; AAA31156.1; -; mRNA.
 DR EMBL; V00876; CAA24245.1; -; mRNA.

DR EMBL; V00877; CAA24246.1; -; mRNA.
 DR PIR; A92444; ADREA.
 DR PDB; IADO; X-ray; A/B/C/D=1-363.
 DR PDB; IEMD; X-ray; A/B/C/D=1-363.
 DR PDB; IEMG; X-ray; A/B/C/D=1-363.
 DR PDB; IEMG; X-ray; A/B/C/D=1-363.
 DR PDB; IEMX; X-ray; A/B/C/D=1-363.
 DR PDB; IJ4E; X-ray; A/B/C/D=1-363.
 DR PDB; IZAH; X-ray; A/B/C/D=1-363.
 DR PDB; IZAI; X-ray; A/B/C/D=1-363.
 DR PDB; IZAJ; X-ray; A/B/C/D=1-363.
 DR PDB; IZAL; X-ray; A/B/C/D=1-363.
 DR PDB; IZALD; X-ray; A/B/C/D=1-363.
 DR InterPro; IPR000741; Aldolase_I.
 DR PANTHER; PTHR11627; Aldolase_I; 1.
 DR Pfam; PF00274; Glycolytic; 1.
 DR ProDom; PD001128; Aldolase_I; 1.
 DR PROSITE; PS00158; ALDOLASE_CLASS_I; 1.
 KW 3D-structure; Direct protein sequencing; Glycolysis; Lyase;
 Multigene family; Schiff base.
 FT INIT_MET 0
 FT ACT_SITE 187 187
 FT ACT_SITE 229 229
 FT BINDING 42 42
 FT BINDING 303 303
 FT SITE 72 72
 FT SITE 107 107
 FT SITE 146 146
 FT SITE 361 361
 FT SITE 363 363
 FT MOD_RES 360 360
 FT MUTAGEN 34 34
 FT MUTAGEN 42 42
 FT MUTAGEN 146 146
 FT MUTAGEN 187 187
 FT MUTAGEN 187 187
 FT MUTAGEN 189 189
 FT MUTAGEN 229 229
 FT MUTAGEN 303 303
 FT CONFLICT 34 34
 FT CONFLICT 273 275
 FT CONFLICT 293 295
 FT CONFLICT 353 353
 FT HELIX 9 22
 FT TURN 23 23
 FT TURN 25 26
 FT STRAND 28 32
 FT HELIX 36 45
 FT TURN 46 47
 FT HELIX 52 63
 FT TURN 64 64
 FT HELIX 67 72
 FT STRAND 73 78
 FT HELIX 80 83
 FT TURN 84 84
 FT STRAND 86 86
 FT TURN 88 89
 FT STRAND 92 92
 FT HELIX 93 99
 FT TURN 100 101
 FT STRAND 103 107
 FT STRAND 112 114
 FT TURN 116 117
 FT STRAND 122 124
 FT TURN 128 129
 FT HELIX 130 139

Proton acceptor.
 Schiff-base intermediate with
 dihydroxyacetone-P.
 Substrate; C-6-phosphate group,
 alkylation inactivates the enzyme.
 Substrate; C-6-phosphate group.
 Essential for substrate cleavage.
 Essential for substrate cleavage.
 Alkylation inactivates the enzyme.
 Alkylation inactivates the enzyme;
 essential for the subsequent hydrolysis
 of the dihydroxyacetone Schiff base.
 Necessary for preference for fructose
 1,6-bisphosphate over fructose 1-
 phosphate.
 Deamidated asparagine (in beta chain).
 E->A: Reduces activity 14-fold.
 R->A: Reduces activity 14-fold.
 K->A: Loss of activity.
 E->A: Reduces activity over 100-fold.
 E->Q: Reduces activity over 1000-fold.
 E->Q: Reduces activity 20-fold.
 R->M: Loss of activity.
 R->A: Reduces activity 400-fold.
 E -> Q (in Ref. 3).
 QQS -> SQE (in Ref. 5).
 S -> E (in Ref. 5).
 KPW -> WPK (in Ref. 5).
 S -> R (in Ref. 6).

FT TURN 140 141
 FT STRAND 144 151

Query Match 100.0%; Score 100; DB 1; Length 363;
 Best Local Similarity 100.0%; Pred. No. 8.3e-08;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSGQAGAAASLSLFTSNHAY 20
 |||||
 DB 344 PSGQAGAAASLSLFTSNHAY 363

RESULT 2
 Q9BWD9 HUMAN PRELIMINARY; PRT; 260 AA.

ID Q9BWD9 HUMAN PRELIMINARY; PRT; 260 AA.
 AC Q9BWD9; Q96B15;
 DT 01-JUN-2001 (TREMELrel. 17, Created)
 DT 01-MAR-2004 (TREMELrel. 26, Last sequence update)
 DT 10-MAY-2005 (TREMELrel. 30, Last annotation update)
 DE ALDOA protein (Similar to aldolase A, fructose-bisphosphate) (Fragment).
 DE Name=ALDOA;
 GN Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=lung;
 RX MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.M., Bhat N.K.,
 RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
 RA Diatchenko L., Marushina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Pahey J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting J., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=lung;
 RA Strausberg R.;
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=lung;
 RA Strausberg R.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- INTERACTION:
 CC Q86WS7;-; NbExp1; IntAct=EBI-373607, EBI-372406;
 DR EMBL; BC000367; AAH00367.2; -; mRNA.
 DR EMBL; BC016170; AAH16170.1; -; mRNA.
 DR HSP; F04075; IALD.
 DR SMR; Q9BWD9; 1-260.
 DR IntAct; Q9BWD9; -;
 DR GO; GO:0004332; F:fructose-bisphosphate aldolase activity; IEA.
 DR GO; GO:0016829; F:lyase activity; IEA.
 DR GO; GO:0006096; P:glycolysis; IEA.
 DR InterPro; IPR000741; Aldolase_1.
 DR Pfam; PF00274; Glycolytic; 1.

DR ProDom; PD001128; Aldolase_I; 1.
 DR PROSITE; PS00158; ALDOLASE_CLASS_I; UNKNOWN_1.
 KW Glycolysis; Lyase.
 FT NON_TER 1
 SQ SEQUENCE 260 AA; 27898 MW; 861B9CDE0F1P2784 CRC64;

Query Match 99.0%; Score 99; DB 2; Length 260;
 Best Local Similarity 95.0%; Pred. No. 8.4e-08;
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSGQAGAAASLSLFTSNHAY 20
 |||||
 DB 241 PSGQAGAAASLSLFTSNHAY 260

RESULT 3
 ALDOA HUMAN STANDARD; PRT; 363 AA.

ID ALDOA HUMAN STANDARD; PRT; 363 AA.
 AC P04075; Q5FH76;
 DT 01-NOV-1986 (Rel. 03, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Muscle-type aldolase)
 DE (Lung cancer antigen NY-LU-1).
 GN Name=ALDOA; Synonyms=ALDA;
 OS Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=85306986; PubMed=3840020;
 RA Sakakibara M., Mukai T., Hori K.;
 RT "Nucleotide sequence of a cDNA clone for human aldolase: a messenger
 RT RNA in the liver."
 RL Biochem. Biophys. Res. Commun. 131:413-420 (1985).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Fibroblast;
 RX MEDLINE=87161904; PubMed=3030757;
 RA Izzo P., Costanzo P., Lupo A., Rippa E., Borghese A.M., Paoletta G.,
 RA Salvatore F.;
 RT "A new human species of aldolase A mRNA from fibroblasts."
 RL Eur. J. Biochem. 164:9-13 (1987).
 RN [3]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=88183272; PubMed=3355497;
 RA Freemont P.S., Dunbar B., Fothergill-Gilmore L.A.;
 RT "The complete amino acid sequence of human skeletal-muscle fructose-
 RT bisphosphate aldolase."
 RL Biochem. J. 249:779-788 (1988).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=88271327; PubMed=3391172;
 RA Izzo P., Costanzo P., Lupo A., Rippa E., Paoletta G., Salvatore F.;
 RT "Human aldolase A gene. Structural organization and tissue-specific
 RT expression by multiple promoters and alternate mRNA processing."
 RL Eur. J. Biochem. 174:569-578 (1988).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=91153319; PubMed=1999195;
 RA Mukai T., Arai Y., Yatsuki H., Joh K., Hori K.;
 RT "An additional promoter functions in the human aldolase A gene, but
 RT not in rat."
 RL Eur. J. Biochem. 195:781-787 (1991).
 RN [6]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RA Ebert L., Schick M., Neubert P., Schattner R., Henze S., Korn B.;
 RT "Cloning of human full open reading frames in Gateway(TM) system entry
 RT vector (pDONR201)."
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

RN [7] NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Cervix, Eye, Lung, Testis, and Uterus;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altchul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gnaratne P.H.S.,
 RA Richards S., Worley K.C., Hale S.E., Garcia A.L., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [8]
 RP PROTEIN SEQUENCE OF 1-62 AND 147-357.
 RX MEDLINE=84126818; PubMed=6696436;
 RA Freemont P.S., Dunbar B., Fothergill L.A.;
 RT "Human skeletal-muscle aldolase: N-terminal sequence analysis of CNBr-
 and o-iodobenzoic acid-cleavage fragments.";
 RL Arch. Biochem. Biophys. 228:342-352(1984).
 RN [9]
 RP NUCLEOTIDE SEQUENCE OF 1-107.
 RX MEDLINE=88155643; PubMed=3441006;
 RA Maite P., Gautron S., Hakim V., Gregori C., Mennecier F., Kahn A.;
 RT "Characterization of three optional promoters in the 5' region of the
 human aldolase A gene.";
 RL J. Mol. Biol. 197:425-438(1987).
 RN [10]
 RP PROTEIN SEQUENCE OF 1-21.
 RX TISSUE=Platelet;
 RC MEDLINE=22608298; PubMed=12665801; DOI=10.1038/nbt810;
 RA Gevaert K., Goethals M., Martens L., Van Damme J., Staes A.,
 RA Thomas G.R., Vandekerckhove J.;
 RT "Exploring proteomes and analyzing protein processing by mass
 spectrometric identification of sorted N-terminal peptides.";
 RL Nat. Biotechnol. 21:566-569(2003).
 RN [11]
 RP NUCLEOTIDE SEQUENCE OF 138-363.
 RX MEDLINE=88046782; PubMed=3674018;
 RA Tolan D.R., Nicolas J., Bruce B.D., Lebo R.V.;
 RT "Evolutionary implications of the human aldolase-A, -B, -C, and -
 pseudogene chromosome locations.";
 RL Am. J. Hum. Genet. 41:907-924(1987).
 RN [12]
 RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
 RX MEDLINE=90242948; PubMed=2532208; DOI=10.1016/0014-5793(90)80211-Z;
 RA Gamblin S.J., Cooper B., Millar J.R., Davies G.J., Littlechild J.A.,
 RA Watson H.C.;
 RT "The crystal structure of human muscle aldolase at 3.0-A resolution.";
 RL FEBS Lett. 262:282-286(1990).
 RN [13]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RX MEDLINE=91278081; PubMed=2056525;
 RA Gamblin S.J., Davies G.J., Grimes J.M., Jackson R.M.,
 RA Littlechild J.A., Watson H.C.;
 RT "Activity and specificity of human aldolases.";
 RL J. Mol. Biol. 219:573-576(1991).
 RN [14]
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
 RX MEDLINE=99156067; PubMed=10048322;
 RA Dalby A., Dauter Z., Littlechild J.A.;
 RT "Crystal structure of human muscle aldolase complexed with fructose

RT 1,6-bisphosphate; mechanistic implications.";
 RL Protein Sci. 8:291-297(1999).
 RN [15]
 RP VARIANT HEMOLYTIC ANEMIA GLY-128.
 RX MEDLINE=89068641; PubMed=2825199;
 RA Kishi H., Mukai T., Hirono A., Fujii H., Miwa S., Hori K.;
 RT "Human aldolase A deficiency associated with a hemolytic anemia:
 thermolabile aldolase due to a single base mutation.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:8623-8627(1987).
 RN [16]
 RP VARIANT HEMOLYTIC ANEMIA GLY-128.
 RX MEDLINE=91035340; PubMed=2229018;
 RA Takasaki Y., Takahashi I., Mukai T., Hori K.;
 RT "Human aldolase A of a hemolytic anemia patient with Asp-128-->Gly
 substitution: characteristics of an enzyme generated in E. coli
 transfected with the expression plasmid PHAD128G.";
 RL J. Biochem. 108:153-157(1990).
 CC -|- CATALYTIC ACTIVITY: D-fructose 1,6-bisphosphate = glycetone
 phosphate + D-glyceraldehyde 3-phosphate.
 CC -|- PATHWAY: Glycolysis; sixth step.
 CC -|- SUBUNIT: Homotetramer.
 CC -|- DISEASE: Defects in ALDOA are a cause of hemolytic anemia
 [MIM:103850].
 CC -|- MISCELLANEOUS: In vertebrates, three forms of this ubiquitous
 glycolytic enzyme are found, aldolase A in muscle, aldolase B in
 liver and aldolase C in brain.
 CC -|- SIMILARITY: Belongs to the class I fructose-bisphosphate aldolase
 family.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use as long as its content is in no way modified and this statement is not
 removed.
 CC EMBL; M11560; AAA51690.1; -; mRNA.
 DR EMBL; X05236; CAA28861.1; -; mRNA.
 DR EMBL; X12447; CAA30979.1; ALT_SEQ; Genomic_DNA.
 DR EMBL; CR541880; CAG46678.1; -; mRNA.
 DR EMBL; BC004333; AAH04333.1; -; mRNA.
 DR EMBL; BC010660; AAH10660.1; -; mRNA.
 DR EMBL; BC012880; AAH12880.1; -; mRNA.
 DR EMBL; BC013614; AAH13614.1; -; mRNA.
 DR EMBL; BC015888; AAH15888.1; -; mRNA.
 DR EMBL; BC016800; AAH16800.1; -; mRNA.
 DR EMBL; X06352; CAA29654.1; -; Genomic_DNA.
 DR EMBL; M21190; AAA51697.1; -; mRNA.
 DR PIR; S14084; ADHUA.
 DR PDB; 1ALD; X-ray; @=1-363.
 DR PDB; 2ALD; X-ray; A=1-363.
 DR PDB; 4ALD; X-ray; @=1-363.
 DR SWISS-2DPAGE; P04075; HUMAN.
 DR Aarhus/Ghent-2DPAGE; 1302; NEPHGE.
 DR OGP; P04075; -.
 DR Siena-2DPAGE; P04075; -.
 DR Ensembl; ENSG00000149925; Homo sapiens.
 DR HGNC; HGNC:414; ALDOA.
 DR H-InvDB; HIX0012935; -.
 DR Reactome; P04075; -.
 DR MIM; 103850; -.
 DR GO; GO:0004332; F:fructose-bisphosphate aldolase activity; TAS.
 DR GO; GO:0006000; P:fructose metabolism; TAS.
 DR GO; GO:0006096; P:glycolysis; TAS.
 DR GO; GO:0006941; P:striated muscle contraction; TAS.
 DR InterPro; IPR000741; Aldolase I.
 DR PANTHER; PTHR11627; Aldolase I.
 DR Pfam; PF00274; Glycolytic; 1.
 DR Prodom; PD001128; Aldolase_1; 1.
 DR PROSITE; PS00158; ALDOLASE_CLASS_I; 1.
 DR 3D-structure; Direct protein sequencing; Disease mutation; Glycolysis;
 KW Lyase; Multigene family; Schiff base.
 Query Match 99.0%; Score 99; DB 1; Length 363;


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Best Local Similarity 95.0%; Pred. No. 1.2e-07; Mismatches 0; Indels 0; Gaps 0;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQAGAAASESLFVSNHAY 20
    |||||
DB 344 PSQAGAAASESLFVSNHAY 363

RESULT 4
Q6FI10 HUMAN
ID Q6FI10 HUMAN PRELIMINARY; PRT; 364 AA.
AC Q6FI10
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Fructose-bisphosphate aldolase.
GN Name=ALDOA;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Halleck A., Ebert L., Moundinya M., Schick M., Eisenstein S.,
RA Neubert P., Katrang K., Schatten R., Shen B., Henze S., Mar W.,
RA Korn B., Zuo D., Hu Y., Labaer J.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR536528; CAG38765.1; -; mRNA.
DR SMR; Q6FI10; 2-364.
DR GO; GO:0004332; F:fructose-bisphosphate aldolase activity; IEA.
DR GO; GO:0006096; P:glycolysis; IEA.
DR InterPro; IPR000741; Aldolase_I.
DR Pfam; PF00274; Glycolytic; 1.
DR PROSITE; PS00158; ALDOLASE_CLASS_I; 1.
KW GLYCOLYSIS; LYASE.
SQ SEQUENCE 364 AA; 39420 MW; 0AAED80F755A7BE8 CRC64;

Query Match 99.0%; Score 99; DB 2; Length 364;
Best Local Similarity 95.0%; Pred. No. 1.2e-07;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQAGAAASESLFVSNHAY 20
    |||||
DB 345 PSQAGAAASESLFVSNHAY 364

RESULT 5
Q5NVR5 PONY
ID Q5NVR5 PONY PRELIMINARY; PRT; 364 AA.
AC Q5NVR5
DT 01-FEB-2005 (TREMBLrel. 29, Created)
DT 01-FEB-2005 (TREMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TREMBLrel. 29, Last annotation update)
DE Fructose-bisphosphate aldolase.
GN Name=DKFPZ470J0811;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RG The German cDNA Consortium;
RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR925940; CAI29598.1; -; mRNA.
DR SMR; Q5NVR5; 2-364.
DR GO; GO:0004332; F:fructose-bisphosphate aldolase activity; IEA.
DR GO; GO:0006096; P:glycolysis; IEA.
DR GO; GO:0006096; P:glycolysis; IEA.
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DR InterPro; IPR000741; Aldolase_I.
DR Pfam; PF00274; Glycolytic; 1.
DR ProDom; PD001128; Aldolase_I; 1.
DR PROSITE; PS00158; ALDOLASE_CLASS_I; 1.
KW GLYCOLYSIS; HYPOTHETICAL PROTEIN; LYASE.
SQ SEQUENCE 364 AA; 39448 MW; 4DAED62BFE37CD33 CRC64;

Query Match 99.0%; Score 99; DB 2; Length 364;
Best Local Similarity 95.0%; Pred. No. 1.2e-07;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQAGAAASESLFVSNHAY 20
    |||||
DB 345 PSQAGAAASESLFVSNHAY 364

RESULT 6
ALDOA MOUSE
ID ALDOA MOUSE STANDARD; PRT; 363 AA.
AC P05064;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Muscle-type aldolase)
DE (Aldolase 1).
GN Name=Aldoa; Synonyms=Aldol;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=129;
EX MEDLINE=88096598; PubMed=3697100;
RA Mestek A., Stauffer J., Tolan D.R., Ciejek-Baez E.;
RT "Sequence of a mouse brain aldolase A cDNA.";
RL Nucleic Acids Res. 15:10595-10595(1987).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=C57BL/6; TISSUE=Brain;
EX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faney J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE OF 1-265 AND 294-363.
EX MEDLINE=90307699; PubMed=2365699;
RA Stauffer J.K., Colbert M.C., Ciejek-Baez E.;
RT "Nonconservative utilization of aldolase A alternative promoters.";
RL J. Biol. Chem. 265:11773-11782(1990).
RN [4]
RP NUCLEOTIDE SEQUENCE OF 98-354.
EX MEDLINE=86192445; PubMed=3009179;
RA Paoletti G., Buono P., Mancini P., Izzo P., Salvatore F.;
RT "Structure and expression of mouse aldolase genes. Brain-specific
```



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RT aldolase C amino acid sequence is closely related to aldolase A.";
RL Eur. J. Biochem. 156:229-235(1986).
CC -!- CATALYTIC ACTIVITY: D-fructose 1,6-bisphosphate = glyceralone
CC phosphate + D-glyceraldehyde 3-phosphate.
CC -!- PATHWAY: Glycolysis; sixth step.
CC -!- SUBUNIT: Homotetramer.
CC -!- MISCELLANEOUS: In vertebrates, three forms of this ubiquitous
CC glycolytic enzyme are found, aldolase A in muscle, aldolase B in
CC liver and aldolase C in brain.
CC -!- SIMILARITY: Belongs to the class I fructose-bisphosphate aldolase
CC family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; X03797; CAA27423.1; -; mRNA.
DR EMBL; BC043026; AAH43026.1; -; mRNA.
DR EMBL; BC050896; AAH50896.1; -; mRNA.
DR EMBL; J05517; AA37210.2; -; Genomic_DNA.
DR EMBL; Y00516; CAA68571.1; -; mRNA.
DR PIR; S06323; ADMSA.
DR HSSP; P00863; IADO.
DR SMR; P05064; 1-363.
DR SWISS-2DPAGE; P05064; MOUSE.
DR Ensembl; ENSMUSG00000030695; Mus musculus.
DR MGI; MGI:87994; Aldoa.
DR GO; GO:0004332; F:fructose-bisphosphate aldolase activity; IDA.
DR InterPro; IPR000741; Aldolase_I.
DR PANTHER; PTHR11627; Aldolase_I; 1.
DR Pfam; PF00274; Glycolytic; 1.
DR ProDom; PD001128; Aldolase_I; 1.
DR PROSITE; PS00158; ALDOLASE_CLASS_I; 1.
KW Glycolysis; Lyase; Multigene family; Schiff base.
FT INIT_MET 0
FT ACT_SITE 187 187 Proton acceptor (By similarity).
FT ACT_SITE 229 229 Schiff-base intermediate with
FT BINDING 55 55 dihydroxyacetone-P.
FT BINDING 146 146 Substrate; C-1-phosphate group.
FT SITE 363 363 Substrate; C-1-phosphate group.
FT 1,6-bisphosphate over fructose 1-
FT CONFLICT 280 280 S -> C (in Ref. 4).
FT SEQUENCE 363 AA; 39225 MW; 62D27089F284BF74 CRC64;

Query Match 97.0%; Score 97; DB 1; Length 363;
Best Local Similarity 95.0%; Pred.No. 2.6e-07;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 P5GQGAASLSLFSINHAY 20
Db 344 P5GQSGAASLSLFSINHAY 363
|||||
P5GQGAASLSLFSINHAY 20
P5GQSGAASLSLFSINHAY 363

RESULT 7
ALDOA RAT
ID ALDOA RAT STANDARD; PRT; 363 AA.
AC P05065; Q63038;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Muscle-type aldolase).
GN Name=Aldoa;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.

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RX MEDLINE=86140113; PubMed=3753977;
RA Mukai T., Joh K., Arai Y., Yatsuki H., Hori K.;
RT "Tissue-specific expression of rat aldolase A mRNAs. Three molecular
RT species differing only in the 5'-terminal sequences.";
RL J. Biol. Chem. 261:3347-3354(1986).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=86081188; PubMed=2416636; DOI=10.1016/0378-1119(85)90102-7;
RA Joh K., Mukai T., Yatsuki H., Hori K.;
RT "Rat aldolase A messenger RNA: the nucleotide sequence and multiple
RT mRNA species with different 5'-terminal regions.";
RL Gene 39:17-24(1985).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=87060996; PubMed=3783705;
RA Joh K., Arai Y., Mukai T., Hori K.;
RT "Expression of three mRNA species from a single rat aldolase A gene,
RT differing in their 5' non-coding regions.";
RL J. Mol. Biol. 190:401-410(1986).
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Prostate;
RG NIH - Mammalian Gene Collection (MGC) project;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
RN [5]
RP NUCLEOTIDE SEQUENCE OF 323-355, AND TISSUE SPECIFICITY.
RC STRAIN=Donryu; TISSUE=Hepatoma;
RX MEDLINE=84261525; PubMed=6086339;
RA Tautumi R., Tautumi K.-I., Numazaki M., Ishikawa K.;
RT "Two different aldolase A mRNA species in rat tissues.";
RL Eur. J. Biochem. 142:161-164(1984).
CC -!- CATALYTIC ACTIVITY: D-fructose 1,6-bisphosphate = glyceralone
CC phosphate + D-glyceraldehyde 3-phosphate.
CC -!- PATHWAY: Glycolysis; sixth step.
CC -!- SUBUNIT: Homotetramer.
CC -!- TISSUE SPECIFICITY: Expressed in muscle, brain and hepatoma cells.
CC -!- MISCELLANEOUS: In vertebrates, three forms of this ubiquitous
CC glycolytic enzyme are found, aldolase A in muscle, aldolase B in
CC liver and aldolase C in brain.
CC -!- SIMILARITY: Belongs to the class I fructose-bisphosphate aldolase
CC family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; M12919; AAA40714.1; -; mRNA.
DR EMBL; M14420; AAA40715.1; -; mRNA.
DR EMBL; X04261; CAA27815.1; -; Genomic_DNA.
DR EMBL; X04262; CAA27815.1; JOINED; Genomic_DNA.
DR EMBL; X04263; CAA27815.1; JOINED; Genomic_DNA.
DR EMBL; X04264; CAA27815.1; JOINED; Genomic_DNA.
DR EMBL; BC064440; AAH64440.1; -; mRNA.
DR EMBL; M28282; AAA40720.1; -; mRNA.
DR PIR; A24532; ADRTA.
DR HSSP; P00883; IADO.
DR SMR; P05065; 1-363.
DR IntAct; P05065; -.
DR Rat-heart-2DPAGE; P05065; -.
DR Ensembl; ENSRNOG00000023647; Rattus norvegicus.
DR RGD; 2089; Aldoa.
DR InterPro; IPR000741; Aldolase_I.
DR PANTHER; PTHR11627; Aldolase_I; 1.
DR Pfam; PF00274; Glycolytic; 1.
DR ProDom; PD001128; Aldolase_I; 1.
DR PROSITE; PS00158; ALDOLASE_CLASS_I; 1.
KW Glycolysis; Lyase; Multigene family; Schiff base.
FT INIT_MET 0
FT ACT_SITE 187 187 Proton acceptor (By similarity).
FT ACT_SITE 229 229 Schiff-base intermediate with
FT dihydroxyacetone-P.

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FT	BINDING	55	55	Substrate; C-1-phosphate group.
FT	BINDING	146	146	Substrate; C-1-phosphate group.
FT	SITE	363	363	Necessary for preference for fructose 1,6-bisphosphate over fructose 1-phosphate.
FT	CONFLICT	144	144	F -> S (in Ref. 2).
FT	CONFLICT	164	164	M -> V (in Ref. 2).
FT	CONFLICT	329	329	K -> Q (in Ref. 5).
SO	SEQUENCE	363 AA; 39221 MW; 48A0468B9E3B9D88 CRC64;		

Query Match 97.0%; Score 97; DB 1; Length 363;
 Best Local Similarity 95.0%; Pred. No. 2.6e-07;
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	1	PSGQGAASSELSFISNHAY 20	
		:	
Db	344	PSGQGAASSELSFISNHAY 363	

RESULT 8

Q5FWB7_MOUSE	Q5FWB7_MOUSE PRELIMINARY;	PRT; 364 AA.
AC	Q5FWB7;	
DT	10-MAY-2005 (TRENBLrel. 30, Created)	
DT	10-MAY-2005 (TRENBLrel. 30, Last sequence update)	
DT	10-MAY-2005 (TRENBLrel. 30, Last annotation update)	
DE	Aldolase 1, A isoform.	
GN	Name=Aldoa;	
OS	Mus musculus (Mouse);	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;	
OC	Muridae; Murinae; Mus.	
OX	NCBI_TaxID=10090;	
[1]		
RP	NUCLEOTIDE SEQUENCE.	
RC	TISSUE=Kidney;	
RC	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;	
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,	
RA	Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D.,	
RA	Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,	
RA	Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J.J., Hsieh F.,	
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,	
RA	Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,	
RA	Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,	
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,	
RA	Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,	
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,	
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	
RA	Fahney J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,	
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,	
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,	
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,	
RA	Butterfield Y.S.N., Krywinski M.I., Skalska U., Smalls D.B.,	
RA	Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;	
RT	"generation and initial analysis of more than 15,000 full-length human	
RT	and mouse cDNA sequences."	
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).	
RL	[2]	
RP	NUCLEOTIDE SEQUENCE.	
RC	TISSUE=Kidney;	
RC	Director MGC Project;	
RL	Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; BC089495; AAH89495.1; -, mRNA.	
DR	MGI; MGI.187894; Aldoa.	
DR	GO; GO:0004332; L:fructose-bisphosphate aldolase activity; IDA.	
KW	Glycolysis; Lyase.	
SO	SEQUENCE 364 AA; 39356 MW; 0D067F784C63E216 CRC64;	

Query Match 97.0%; Score 97; DB 2; Length 364;
 Best Local Similarity 95.0%; Pred. No. 2.6e-07;
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	1	PSGQGAASSELSFISNHAY 20	
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RT evolutionary implications.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Osada N., Hirata M., Tanuma R., Kusuda J., Hida M., Suzuki Y.,
RA Sugano S., Gojobori T., Shen J.C.-K., Wu C.I., Hashimoto K.;
RT "Substitution rate and structural divergence of 5'UTR evolution:
RT Comparative analysis between human and cynomolgus monkey CDNAs.";
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB169721; BAE01802.1; -; mRNA.
DR InterPro; IPR000741; Aldolase_I.
DR Pfam; PF00274; Glycolytic; 1.
DR ProDom; PD001128; Aldolase_I; 1.
DR PROSITE; PS00158; ALDOLASE_CLASS_I; UNKNOWN_1.
DR GlycoLySis; Lyase.
SQ SEQUENCE 276 AA; 29587 MW; 2CDF4D877E140C2F CRC64;

Query Match          94.0%; Score 94; DB 2; Length 276;
Best Local Similarity 90.0%; Pred. No. 6e-07;
Matches 18; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PSQGAGAAASESLFISNHAY 20
   ||| ||||| ||||| |||||
Db 257 PSCHAGAAASESLFVSNHAY 276

RESULT 12
Q8WNT7 MACFA
ID Q8WNT7 MACFA PRELIMINARY; PRT; 704 AA.
AC Q8WNT7;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Fructose-1,6-bisphosphate aldolase A.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Testis;
RA Osada N., Hida M., Kusuda J., Tanuma R., Hirata M., Suto Y., Hirai M.,
RA Terao K., Sugano S., Hashimoto K.;
RT "Cynomolgus monkey testicular cDNAs for discovery of novel human genes
RT in the human genome sequence.";
RL BMC Genomics 3:36-36(2002).
DR EMBL; AB066558; BAB84033.1; -; mRNA.
DR HSP; P04075; 2ALD.
DR SMR; Q8WNT7; 342-704.
DR GO; GO:0004332; F:fructose-bisphosphate aldolase activity; IEA.
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0006036; P:glycolysis; IEA.
DR InterPro; IPR000741; Aldolase_I.
DR Pfam; PF00274; Glycolytic; 1.
DR ProDom; PD001128; Aldolase_I; 1.
DR PROSITE; PS00158; ALDOLASE_CLASS_I; UNKNOWN_1.
KW GlycoLySis; Lyase.
SQ SEQUENCE 704 AA; 74686 MW; 02D9A004C37DFF39 CRC64;

Query Match          94.0%; Score 94; DB 2; Length 704;
Best Local Similarity 90.0%; Pred. No. 1.7e-06;
Matches 18; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PSQGAGAAASESLFISNHAY 20
   ||| ||||| ||||| |||||
Db 695 PSCHAGAAASESLFVSNHAY 704

RESULT 13
Q76BG8 AMBME
ID Q76BG8 AMBME PRELIMINARY; PRT; 331 AA.
AC Q76BG8;

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RESULT 10
Q92007 CHICK
ID Q92007 CHICK PRELIMINARY; PRT; 42 AA.
AC Q92007;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-FEB-2005 (TReMBLrel. 29, Last annotation update)
DE Aldolase C (Aldolase A) (Fragment).
GN Name=aldolase C;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95286677; PubMed=7768978;
RA Meighan-Mantha R.L., Tolan D.R.;
RT "Noncoordinate changes in the steady-state mRNA expressed from
RT aldolase A and aldolase C genes during differentiation of chicken
RT myoblasts.";
RL J. Cell. Biochem. 57:423-431(1995).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Muscle;
RA Meighan-Mantha R.L., Tolan D.R.;
RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL; S78288; AAB34479.1; -; mRNA.
DR EMBL; L25374; AAA99864.1; -; mRNA.
DR EMBL; L25373; AAA48588.1; -; mRNA.
DR PIR; I51291; I51291.
DR HSP; P00883; 6ALD.
DR GO; GO:0004332; F:fructose-bisphosphate aldolase activity; IEA.
DR GO; GO:0006096; P:glycolysis; IEA.
DR InterPro; IPR000741; Aldolase_I.
DR Pfam; PF00274; Glycolytic; 1.
FT NON_TER 42
SQ SEQUENCE 42 AA; 4384 MW; 780E34B8C695DC4B CRC64;

Query Match          95.0%; Score 95; DB 2; Length 42;
Best Local Similarity 95.0%; Pred. No. 5.4e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PSQGAGAAASESLFISNHAY 20
   ||| ||||| ||||| |||||
Db 23 PSCHAGAAASESLFISNHAY 42

RESULT 11
Q4RS23 MACFA
ID Q4RS23 MACFA PRELIMINARY; PRT; 276 AA.
AC Q4RS23;
DT 13-SEP-2005 (TReMBLrel. 31, Created)
DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)
DE Brain cDNA, clone: Qf1A-11254, similar to human aldolase A, fructose-
DE bisphosphate (ALDOA), transcript variant 2.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA International consortium for macaque cDNA sequencing, analysis;
RT "DNA sequences of macaque genes expressed in brain or testis and its

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DT 05-JUL-2004 (TREMELrel. 27, Created)
 DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)
 DE Fructose-bisphosphate Aldolase A (Fragment).
 OS Ambystoma mexicanum (Axolotl).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Caudata; Salamandroidae; Ambystomatidae;
 OC Ambystoma.
 OX NCBI_TaxID=8296;
 RN [1]
 RC NUCLEOTIDE SEQUENCE.
 RP TISSUE=Tail;
 RA Kikugawa K., Katoh K., Kuraku S., Sakurai H., Ishida O., Iwabe N.,
 RA Miyata T.;
 RT "Basal jawed vertebrate phylogeny inferred from multiple nuclear DNA-
 RT coded genes.";
 RL BMC Biol. 2:3-3(2004).
 DR EMBL; AB111374; RAD1788.1; -; mRNA.
 DR HSSP; P04075; 1ALD.
 DR SMR; Q76BG8; 1-331.
 DR GO; GO:0004332; F:fructose-bisphosphate aldolase activity; IEA.
 DR GO; GO:0016829; F:lyase activity; IEA.
 DR GO; GO:0006096; P:glycolysis; IEA.
 DR InterPro; IPR000741; Aldolase_I.
 DR Pfam; PF00274; Glycolytic; 1.
 DR ProDom; PD001128; Aldolase_I; 1.
 DR PROSITE; PS00158; ALDOLASE_CLASS_I; 1.
 KW Glycolysis; Lyase.
 FT NON TER 1
 SQ SEQUENCE 331 AA; 36170 MW; B7374F829DE6C591 CRC64;
 Query Match 89.0%; Score 89; DB 2; Length 331;
 Best Local Similarity 85.0%; Pred. No. 4.9e-06;
 Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 PSQAQGAASESLFVSNHAY 20
 DB 312 PSQAQGAASESLFVSNHAY 331
 RESULT 14
 Q9CQ09 MOUSE
 ID Q9CQ09 MOUSE PRELIMINARY; PRT; 364 AA.
 AC Q9CQ09;
 DT 01-JUN-2001 (TREMELrel. 17, Created)
 DT 01-JUN-2001 (TREMELrel. 17, Last sequence update)
 DT 01-FEB-2005 (TREMELrel. 29, Last annotation update)
 DE Mus musculus adult male testis cDNA, RIKEN full-length enriched
 DE library, clone:4933417120 product:FRUCTOSE-BISPHOSPHATE ALDOLASE A
 DE (EC 4.1.2.13) (MUSCLE-TYPE ALDOLASE) homolog (Mus musculus adult male
 DE testis cDNA, RIKEN full-length enriched library, clone:4921524E03
 DE product:FRUCTOSE-BISPHOSPHATE ALDOLASE A (EC 4.1.2.13) (MUSCLE-TYPE
 DE ALDOLASE) homolog) (Novel protein similar to aldolase 1, A isoform
 DE Aldol).
 GN Name=Aldoa; Synonyms=Aldol, RP24-191C1.1; ORFNames=RP24-191C1.1-001;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RC NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RC NUCLEOTIDE SEQUENCE.
 RX MEDLINE=21085860; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Pleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Mateu Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli P., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RP [3]
 RC NUCLEOTIDE SEQUENCE.
 RX STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaide I., Oeato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Hammond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
 RA Ravasi T., Reed J.C., Reid J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Sempke C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavanian M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RP [4]
 RC NUCLEOTIDE SEQUENCE.
 RX STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=20493974; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RP [5]
 RC NUCLEOTIDE SEQUENCE.
 RX STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multichannel sequencer.";

RT *RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.*;
 RL Genome Res. 10:1757-1771 (2000).

RN [6]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Testis;
 RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
 RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
 RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
 RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
 RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
 RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
 RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
 RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
 RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
 RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
 RA Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK016920; BAB30498.1; -; mRNA.
 DR EMBL; AK006425; BAB24582.1; -; mRNA.
 DR HSSP; P04075; 2ALD.
 DR SMR; Q9CRCL; 3-364.
 DR Ensembl; ENSMUSG00000063129; Mus musculus.
 DR GO; GO:0004332; P:fructose-bisphosphate aldolase activity; IEA.
 DR GO; GO:0016823; P:lyase activity; IEA.
 DR GO; GO:0006096; P:glycolysis; IEA.
 DR InterPro; IPR000741; Aldolase_I.
 DR Pfam; PF00274; Glycolytic; 1.
 DR ProDom; PD001128; Aldolase_I; 1.
 DR PROSITE; PS00158; ALDOLASE_CLASS_I; 1.
 KW Glycolysis; Lyase.
 SQ SEQUENCE 364 AA; 39370 MW; 0360CD12B8509A0D CRC64;

Query Match 88.0%; Score 88; DB 2; Length 364;
 Best Local Similarity 85.0%; Pred. No. 8e-06;

Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 PSGQAGAAASESLFISNHAY 20

Db 345 PSNESGAAASESLFISNHAY 364

Search completed: February 10, 2006, 10:12:47
 Job time : 17.9004 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 10, 2006, 10:13:09 ; Search time 3.99524 Seconds
(without alignments)
414.909 Million cell updates/sec

Title: US-10-717-243-57

Perfect score: 100

Sequence: 1 PSQQAARASELFINSHAY 20

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgm2_6/ptodata/1/iaa/5_COMB.pep.*
- 2: /cgm2_6/ptodata/1/iaa/6_COMB.pep.*
- 3: /cgm2_6/ptodata/1/iaa/H_COMB.pep.*
- 4: /cgm2_6/ptodata/1/iaa/PCrUS_COMB.pep.*
- 5: /cgm2_6/ptodata/1/iaa/RE_COMB.pep.*
- 6: /cgm2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	100	100.0	20	1	US-07-988-430-59
2	100	100.0	20	1	US-08-425-336-57
3	100	100.0	20	1	US-08-488-113B-57
4	100	100.0	20	1	US-08-477-484B-57
5	100	100.0	20	1	US-08-646-360-57
6	100	100.0	20	2	US-08-839-765-57
7	100	100.0	20	2	US-09-136-389-57
8	100	100.0	20	2	US-08-610-838-57
9	100	100.0	20	2	US-09-711-485-57
10	100	100.0	20	4	PCT-US92-09487-59
11	99	99.0	364	2	US-09-919-039-343
12	99	99.0	419	2	US-09-949-016-8781
13	68	68.0	364	2	US-09-976-594-390
14	46	46.0	170	2	US-09-583-110-3353
15	46	46.0	171	2	US-09-107-433-3864
16	46	46.0	377	2	US-09-949-016-9474
17	45	45.0	659	2	US-09-228-986-75
18	45	45.0	659	2	US-10-101-464A-75
19	45	45.0	736	2	US-09-252-931A-21498
20	44	44.0	176	2	US-09-252-991A-29061
21	44	44.0	863	2	US-09-252-991A-21831
22	43	43.0	200	2	US-09-540-236-3005
23	43	43.0	253	2	US-09-530-058-6
24	43	43.0	593	2	US-09-252-931A-23340
25	43	43.0	697	2	US-09-949-016-9660
26	42	42.0	277	2	US-09-710-279-2802
27	42	42.0	278	2	US-09-252-991A-26039

Sequence 2, Appli
Sequence 2, Appli
Sequence 6776, Ap
Sequence 6359, Ap
Sequence 3542, Ap
Sequence 3106, Ap
Sequence 36667, A
Sequence 51884, A
Sequence 38, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 42299, A
Sequence 47516, A
Sequence 8551, Ap
Sequence 21, Appli
Sequence 13251, A
Sequence 6131, Ap
Sequence 6495, Ap

28 42 42.0 461 2 US-09-122-210-2
29 42 42.0 461 2 US-09-443-681-2
30 42 42.0 626 2 US-09-949-016-6776
31 42 42.0 732 2 US-09-134-000C-6359
32 42 42.0 1017 2 US-09-134-001C-3542
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35 41 41.0 139 2 US-09-270-767-51884
36 41 41.0 244 2 US-09-068-804-38
37 40 40.0 154 1 US-08-449-644-7
38 40 40.0 154 1 US-08-087-244A-7
39 40 40.0 304 2 US-09-270-767-32299
40 40 40.0 304 2 US-09-270-767-47516
41 40 40.0 426 2 US-09-489-039A-8551
42 40 40.0 449 3 US-09-041-075A-21
43 40 40.0 498 2 US-09-489-039A-13251
44 40 40.0 708 2 US-09-328-352-6131
45 40 40.0 715 2 US-09-949-016-6495

ALIGNMENTS

RESULT 1
US-07-988-430-59
; Sequence 59, Application US/07988430
; Patent No. 5416202
; GENERAL INFORMATION:
; APPLICANT: Bernhard, Susan L.
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Lane, Julie A.
; APPLICANT: Lei, Shau-Ping
; TITLE OF INVENTION: Materials Comprising and Methods of
; TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/988,430
; FILING DATE: 19921209
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5416202and, Greta E.
; REGISTRATION NUMBER: 35302
; REFERENCE/DOCKET NUMBER: 31133
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-07-988-430-59

Query Match 100.0%; Score 100; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSQGAAGAAASESLFISNHAY 20
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Db 1 PSQGAAGAAASESLFISNHAY 20

RESULT 2

US-08-425-336-57

; Sequence 57, Application US/08425336
; Patent No. 5621083
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/425,336
; FILING DATE: 18-APR-1995
; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/064,691

; FILING DATE: 12-MAY-1993

; APPLICATION NUMBER: US 07/901,707

; FILING DATE: 19-JUN-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/787,567

; FILING DATE: 04-NOV-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Meyers, Thomas C.

; REGISTRATION NUMBER: P-36,989

; REFERENCE/DOCKET NUMBER: 31394

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 312/474-6300

; TELEFAX: 312/474-0448

; TELEX: 25-3856

; INFORMATION FOR SEQ ID NO: 57:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 20 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-425-336-57

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Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSQGAAGAAASESLFISNHAY 20

Db 1 PSQGAAGAAASESLFISNHAY 20

RESULT 3

US-08-488-113B-57

; Sequence 57, Application US/08488113B
; Patent No. 5744580
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/488,113B

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/425,336

; FILING DATE: 18-APR-1995

; APPLICATION NUMBER: US 08/064,691

; FILING DATE: 12-MAY-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/988,430

; FILING DATE: 09-DEC-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/901,707

; FILING DATE: 19-JUN-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/787,567

; FILING DATE: 04-NOV-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: McNicholas, Janet M.

; REGISTRATION NUMBER: 32,918

; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 312/707-8889

; TELEFAX: 312/707-9155

; TELEX: 650 388-1248

; INFORMATION FOR SEQ ID NO: 57:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 20 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-488-113B-57

Query Match 100.0%; Score 100; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSQGAAGAAASESLFISNHAY 20

Db 1 PSQGAAGAAASESLFISNHAY 20

RESULT 4

US-08-477-484B-57

; Sequence 57, Application US/08477484B
; Patent No. 5756699
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.

APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,484B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-477-484B-57
Query Match 100.0%; Score 100; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 PSGQAGAAASLSLFSNHAY 20
Db 1 PSGQAGAAASLSLFSNHAY 20
RESULT 5
US-08-646-360-57
Sequence 57, Application US/08646360
Patent No. 5837491
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.

STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-646-360-57
Query Match 100.0%; Score 100; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 PSGQAGAAASLSLFSNHAY 20
Db 1 PSGQAGAAASLSLFSNHAY 20
RESULT 6
US-08-839-765-57
Sequence 57, Application US/08839765
Patent No. 6146631
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:


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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/839,765
; FILING DATE: 15-APR-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
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; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-839-765-57
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Query Match 100.0%; Score 100; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 PSGQAGAAASESLFISNHAY 20
Db 1 PSGQAGAAASESLFISNHAY 20
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US-09-136-389-57
; Sequence 57, Application US/09136389
; Patent No. 6146850
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/136,389
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; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-136-389-57
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Query Match 100.0%; Score 100; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 PSGQAGAAASESLFISNHAY 20
Db 1 PSGQAGAAASESLFISNHAY 20
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RESULT 8
US-09-610-838-57
; Sequence 57, Application US/09610838
; Patent No. 6376217
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/610,838
; FILING DATE: 06-JUL-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/136,389
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;; FILING DATE: 18-AUG-1998
;; APPLICATION NUMBER: 08/646,360
;; FILING DATE: 13-MAY-1996
;; APPLICATION NUMBER: PCT/US94/05348
;; FILING DATE: 12-MAY-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/064,691
;; FILING DATE: 12-MAY-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/988,430
;; FILING DATE: 09-DEC-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/901,707
;; FILING DATE: 19-JUN-1992
;; APPLICATION NUMBER: US 07/787,567
;; FILING DATE: 04-NOV-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: McNicholas, Janet M.
;; REGISTRATION NUMBER: 32,918
;; REFERENCE/DOCKET NUMBER: 200-70.P4
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312/707-8889
;; TELEFAX: 312/707-9155
;; TELEX: 650 388-1248
;; INFORMATION FOR SEQ ID NO: 57:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-09-610-838-57

Query Match 100.0%; Score 100; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSGQAGAAASESLFISNHAY 20
Db 1 PSGQAGAAASESLFISNHAY 20

RESULT 9
US-09-711-485-57
; Sequence 57, Application US/09711485
; Patent No. 6649742
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/711.485
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/839,765
; FILING DATE:
; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 08/064,691
;; FILING DATE: 12-MAY-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/988,430
;; FILING DATE: 09-DEC-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/901,707
;; FILING DATE: 19-JUN-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/787,567
;; FILING DATE: 04-NOV-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: McNicholas, Janet M.
;; REGISTRATION NUMBER: 32,918
;; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312/707-8889
;; TELEFAX: 312/707-9155
;; TELEX: 650 388-1248
;; INFORMATION FOR SEQ ID NO: 57:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-09-711-485-57

Query Match 100.0%; Score 100; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSGQAGAAASESLFISNHAY 20
Db 1 PSGQAGAAASESLFISNHAY 20

RESULT 10

PCT-US92-09487-59
; Sequence 59, Application PC/TUS9209487
; GENERAL INFORMATION:
; APPLICANT: Bernhard, Susan L.
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Lane, Julie A.
; APPLICANT: Lei, Shau-Ping
; TITLE OF INVENTION: Materials Comprising and Methods of
; TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/09487
; FILING DATE: 19921104
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:

Query Match 46.0%; Score 46; DB 2; Length 170;
Best Local Similarity 52.4%; Pred. No. 4.6;
Matches 11; Conservative 0; Mismatches 8; Indels 2; Gaps 1;

Qy 2 SQAGAAASE--SLFISNHAY 20
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Db 42 SQAGVVCQEPADFFESNHL 62

RESULT 15
US-09-107-433-3864
; Sequence 3864, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGNOSTIC THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/ 085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 3864:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 171 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...171
; SEQUENCE DESCRIPTION: SEQ ID NO: 3864:
US-09-107-433-3864

Query Match 46.0%; Score 46; DB 2; Length 171;
Best Local Similarity 52.4%; Pred. No. 4.6;
Matches 11; Conservative 0; Mismatches 8; Indels 2; Gaps 1;

Qy 2 SQAGAAASE--SLFISNHAY 20
||||| |
Db 43 SQAGVVCQEPADFFESNHL 63

Search completed: February 10, 2006, 10:15:58
Job time : 3.98524 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 10, 2006, 10:37:59 ; Search time 13.0627 Seconds
(without alignments)
639.727 Million cell updates/sec

Title: US-10-717-243-57

Perfect score: 100

Sequence: 1 PSQQAASLFTSNHAY 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:*

- 1: /cgm2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgm2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 3: /cgm2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 4: /cgm2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 5: /cgm2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 6: /cgm2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	100	100.0	20	4	US-10-127-890-57
2	100	100.0	20	5	Sequence 57, Appl
3	99	99.0	153	4	US-10-717-243-57
4	99	99.0	364	3	US-10-264-049-3838
5	99	99.0	364	4	US-09-919-039-343
6	99	99.0	364	5	US-10-408-765A-537
7	97	97.0	364	5	US-10-370-715B-532
8	96	96.0	112	4	US-10-205-219-67
9	95	95.0	31	3	US-10-425-115-196160
10	68	68.0	364	4	US-10-170-385-259
11	68	68.0	364	4	US-10-408-765A-98
12	61	61.0	365	4	US-10-369-493-5923
13	55.5	55.5	361	4	US-10-108-605-255
14	55.5	55.5	361	6	US-11-097-143-27699
15	52	52.0	366	4	US-10-369-493-5735
16	51	51.0	358	4	US-10-767-701-46629
17	51	51.0	361	4	US-10-425-115-269098
18	51	51.0	371	4	US-10-425-114-65982
19	51	51.0	371	4	US-10-425-115-269100
20	50.5	50.5	215	4	US-10-029-386-33867
21	50.5	50.5	836	4	US-10-108-260A-3700
22	47	47.0	1223	6	US-11-097-143-16989
23	46	46.0	98	4	US-10-424-599-161041
24	46	46.0	132	4	US-10-484-364-2
25	46	46.0	170	5	US-10-472-928-3140
26	46	46.0	171	5	US-10-617-320-3864
27	46	46.0	332	4	US-10-425-114-44042

28 46 46.0 355 4 US-10-425-114-44220 Sequence 44220, A
29 46 46.0 355 4 US-10-425-114-45677 Sequence 45677, A
30 46 46.0 358 4 US-10-424-599-222971 Sequence 222971, A
31 46 46.0 364 4 US-10-177-293-8 Sequence 8, Appli
32 46 46.0 372 4 US-10-425-114-43852 Sequence 43852, A
33 46 46.0 372 4 US-10-425-114-44097 Sequence 44097, A
34 46 46.0 372 4 US-10-425-114-44837 Sequence 44837, A
35 46 46.0 375 4 US-10-425-114-45592 Sequence 45592, A
36 46 46.0 375 4 US-10-425-114-51423 Sequence 51423, A
37 46 46.0 375 4 US-10-425-114-55978 Sequence 55978, A
38 46 46.0 375 4 US-10-425-114-55981 Sequence 55981, A
39 46 46.0 392 4 US-10-437-963-151748 Sequence 151748, A
40 46 46.0 416 4 US-10-437-963-180885 Sequence 180885, A
41 46 46.0 644 4 US-10-408-765A-1196 Sequence 1196, Ap
42 46 46.0 902 4 US-10-029-386-32110 Sequence 32110, A
43 45.5 45.5 388 4 US-10-767-701-46406 Sequence 46406, A
44 45.5 45.5 404 4 US-10-425-115-351374 Sequence 351374, A
45 45.5 45.5 414 4 US-10-425-114-70495 Sequence 70495, A

ALIGNMENTS

RESULT 1

US-10-127-890-57
; Sequence 57, Application US/10127890
; Publication No. US20030166196A1

GENERAL INFORMATION:

APPLICANT: Better, Marc D.
Carroll, Stephen F.
Studnicka, Gary M.

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating Proteins

NUMBER OF SEQUENCES: 173

CORRESPONDENCE ADDRESS:

ADDRESSEE: McAndrews, Held & Malloy, Ltd.

STREET: 500 West Madison Street, 34th floor

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60661

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/127,890

FILING DATE: 23-Apr-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/646,360

FILING DATE: 13-MAY-1996

APPLICATION NUMBER: PCT/US94/05348

FILING DATE: 12-MAY-1994

APPLICATION NUMBER: US 08/064,691

FILING DATE: 12-MAY-1993

APPLICATION NUMBER: US 07/988,430

FILING DATE: 09-DEC-1992

APPLICATION NUMBER: US 07/901,707

FILING DATE: 19-JUN-1992

APPLICATION NUMBER: US 07/787,567

FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:

NAME: McNicholas, Janet M.

REGISTRATION NUMBER: 32,918

REFERENCE/DOCKET NUMBER: 200-70.P4

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/707-8889

TELEFAX: 312/707-9155

TELEX: 650 388-1248

INFORMATION FOR SEQ ID NO: 57:

SEQUENCE CHARACTERISTICS:

;
;
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 57:
US-10-127-890-57

Query Match 100.0%; Score 100; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.9e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQGAGAAASESLFISNHAY 20
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Db 1 PSQGAGAAASESLFISNHAY 20

RESULT 2

US-10-717-243-57
; Sequence 57, Application US/10717243
; Publication No. US20050054835A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Carroll, Stephen F.
; Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/717,243
FILING DATE: 18-Nov-2003
CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/839,765
FILING DATE: 15-APR-1997
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 57:
US-10-717-243-57

Query Match 100.0%; Score 100; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.9e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQGAGAAASESLFISNHAY 20
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Db 1 PSQGAGAAASESLFISNHAY 20

RESULT 3

US-10-264-049-3838
; Sequence 3838, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133P1
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 3838
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-049-3838

Query Match 99.0%; Score 99; DB 4; Length 153;
Best Local Similarity 95.0%; Pred. No. 7.9e-08;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQGAGAAASESLFISNHAY 20
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Db 134 PSQGAGAAASESLFVSNHAY 153

RESULT 4

US-09-919-039-343
; Sequence 343, Application US/09919039
; Publication No. US20030108871A1
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 343
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030108871A1 2706606CD1
US-09-919-039-343

Query Match 99.0%; Score 99; DB 3; Length 364;
Best Local Similarity 95.0%; Pred. No. 2e-07;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQGAGAAASESLFISNHAY 20
|||
Db 345 PSQGAGAAASESLFVSNHAY 364

RESULT 5

US-10-408-765A-537
; Sequence 537, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:

; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Bojin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale B.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04

; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 537
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-537

Query Match 99.0%; Score 99; DB 4; Length 364;
Best Local Similarity 95.0%; Pred. No. 2e-07;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSGQAGAAASLSLFISNHAY 20
|||:|||||:|||||:|||||
DB 345 PSGQAGAAASLSLFVSNHAY 364

RESULT 6

US-10-370-715B-532
; Sequence 532, Application US/10370715B
; Publication No. US20040258678A1
; GENERAL INFORMATION:

; PATIN Docket Preview
; APPLICANT: BODARY, SARAH C.
; APPLICANT: CLARK, HILLARY
; APPLICANT: BRISDELL, HUNTE
; APPLICANT: JACKMAN, JANET
; APPLICANT: SCHOENFELD, JILL R.
; APPLICANT: WILLIAMS, P. MICKEY
; APPLICANT: WOOD, WILLIAM I.
; APPLICANT: WU, THOMAS D.

; TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
; TITLE OF INVENTION: Related Diseases
; FILE REFERENCE: P1948R1-US
; CURRENT APPLICATION NUMBER: US/10/370,715B
; CURRENT FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 742

; SEQ ID NO 532
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-370-715B-532

Query Match 99.0%; Score 99; DB 5; Length 364;
Best Local Similarity 95.0%; Pred. No. 2e-07;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSGQAGAAASLSLFISNHAY 20
|||:|||||:|||||:|||||
DB 345 PSGQAGAAASLSLFVSNHAY 364

RESULT 7

US-10-205-219-67
; Sequence 67, Application US/10205219
; Publication No. US20030138803A1
; GENERAL INFORMATION:

; APPLICANT: Warner-Lambert Company
; APPLICANT: Lee, Kevin
; APPLICANT: Dixon, Alistair
; APPLICANT: Brooksbank, Robert
; APPLICANT: Pinnock, Robert

; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
; FILE REFERENCE: WL-A-018200
; CURRENT APPLICATION NUMBER: US/10/205,219
; CURRENT FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: GB 0118354.0
; PRIOR FILING DATE: 2001-07-27

; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 67
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Aldolase A
US-10-205-219-67

Query Match 97.0%; Score 97; DB 4; Length 364;
Best Local Similarity 95.0%; Pred. No. 4.3e-07;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSGQAGAAASLSLFISNHAY 20
|||:|||||:|||||:|||||
DB 345 PSGQAGAAASLSLFISNHAY 364

RESULT 8

US-10-425-115-196160
; Sequence 196160, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kowalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326

; SEQ ID NO 196160
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Zea mays

; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(112)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MFT4577_110484C.1.pep
US-10-425-115-196160

Query Match 96.0%; Score 96; DB 4; Length 112;
Best Local Similarity 95.0%; Pred. No. 1.7e-07;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PSGQAGAAASLSLFISNHAY 20
|||:|||||:|||||:|||||
DB 93 PSGQAGAAASLSLFISNHAY 112

RESULT 9

US-09-925-301-1462
; Sequence 1462, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:

; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies


```
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 1462
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (13)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-301-1462

Query Match      95.0%; Score 95; DB 3; Length 31;
Best Local Similarity 90.0%; Pred. No. 6.1e-08;
Matches 18; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PSQAGAAASESLFISNHAY 20
Db 12 PXQAGAAASESLFVSNHAY 31

RESULT 10
US-10-170-385-259
; Sequence 259, Application US/10170385
; Publication No. US20030203372A1
; GENERAL INFORMATION:
; APPLICANT: Mundy, Neil Raymond
; APPLICANT: Kan, On
; APPLICANT: Harris, Robert Alan
; APPLICANT: White, Jonathan
; APPLICANT: Binley, Katie Mary
; APPLICANT: Rayner, William Nigel
; APPLICANT: Naylor, Stuart
; APPLICANT: Kingsman, Susan Mary
; APPLICANT: Krige, David
; TITLE OF INVENTION: ANALYSIS METHOD
; FILE REFERENCE: 532682000100
; CURRENT APPLICATION NUMBER: US/10/170,385
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: PCT/GB02/01662
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: PCT/GB01/05458
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 549
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 259
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-170-385-259

Query Match      68.0%; Score 68; DB 4; Length 364;
Best Local Similarity 63.2%; Pred. No. 0.021;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 SQAGAAASESLFISNHAY 20
Db 346 SGEDGAAASQSLYIANHAY 364

RESULT 11
US-10-408-765A-98
; Sequence 98, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Broadus, Julie
; APPLICANT: Stam, Lynn
; APPLICANT: Bachmann, Jane
; APPLICANT: Kamdar, Kim
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE
; TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF
```

```
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Wainock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 98
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-98

Query Match      68.0%; Score 68; DB 4; Length 364;
Best Local Similarity 63.2%; Pred. No. 0.021;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 SQAGAAASESLFISNHAY 20
Db 346 SGEDGAAASQSLYIANHAY 364

RESULT 12
US-10-369-493-5923
; Sequence 5923, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 5923
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-5923

Query Match      61.0%; Score 61; DB 4; Length 365;
Best Local Similarity 68.8%; Pred. No. 0.28;
Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 5 AGAAASESLFISNHAY 20
Db 350 ADAAASQSLFVANHAY 365

RESULT 13
US-10-108-605-255
; Sequence 255, Application US/10108605
; Publication No. US20020160934A1
; GENERAL INFORMATION:
; APPLICANT: Broadus, Julie
; APPLICANT: Stam, Lynn
; APPLICANT: Bachmann, Jane
; APPLICANT: Kamdar, Kim
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE
; TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF
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; FILE REFERENCE: 31133B
 ; CURRENT APPLICATION NUMBER: US/10/108,605
 ; CURRENT FILING DATE: 2002-03-27
 ; PRIOR APPLICATION NUMBER: US 09/761,142
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/176,418
 ; PRIOR FILING DATE: 2000-01-14
 ; NUMBER OF SEQ ID NOS: 361
 ; SOFTWARE: Patent in Ver. 2.1
 ; SEQ ID NO 255
 ; LENGTH: 361
 ; TYPE: PRT
 ; ORGANISM: Drosophila melanogaster
 US-10-108-605-255

Query Match 55.5%; Score 55.5; DB 4; Length 361;
 Best Local Similarity 63.2%; Pred. No. 2.2;
 Matches 12; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

Qy 2 SQGAGAAASESLFISNHAY 20
 :|||||:|||||:
 Db 344 AGSAG-AGGSLFVANHAY 361

RESULT 14

US-11-097-143-27699
 ; Sequence 27699, Application US/11097143
 ; Publication No. US20050208558A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Venter, J. Craig
 ; APPLICANT: et al.
 ; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
 ; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
 ; TITLE OF INVENTION: DROSOPHILA GENES.

; FILE REFERENCE: CL000728
 ; CURRENT APPLICATION NUMBER: US/11/097,143
 ; CURRENT FILING DATE: 2005-04-04
 ; PRIOR APPLICATION NUMBER: 60/157,832
 ; PRIOR FILING DATE: 1999-10-05
 ; PRIOR APPLICATION NUMBER: 60/160,191
 ; PRIOR FILING DATE: 1999-10-19
 ; PRIOR APPLICATION NUMBER: 60/161,932
 ; PRIOR FILING DATE: 1999-10-28
 ; PRIOR APPLICATION NUMBER: 60/164,769
 ; PRIOR FILING DATE: 1999-11-12
 ; PRIOR APPLICATION NUMBER: 60/173,383
 ; PRIOR FILING DATE: 1999-12-28
 ; PRIOR APPLICATION NUMBER: 60/175,693
 ; PRIOR FILING DATE: 2000-01-12
 ; PRIOR APPLICATION NUMBER: 60/184,831
 ; PRIOR FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: 60/191,637
 ; PRIOR FILING DATE: 2000-03-23
 ; NUMBER OF SEQ ID NOS: 43008
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 27699
 ; LENGTH: 361
 ; TYPE: PRT
 ; ORGANISM: DROSOPHILA
 US-11-097-143-27699

Query Match 55.5%; Score 55.5; DB 6; Length 361;
 Best Local Similarity 63.2%; Pred. No. 2.2;
 Matches 12; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

Qy 2 SQGAGAAASESLFISNHAY 20
 :|||||:|||||:
 Db 344 AGSAG-AGGSLFVANHAY 361

RESULT 15

US-10-369-493-5735
 ; Sequence 5735, Application US/10369493

; Publication No. US20030233675A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Chen, Xianfeng
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 ; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
 ; FILE REFERENCE: 38-10(52052)B
 ; CURRENT APPLICATION NUMBER: US/10/369,493
 ; CURRENT FILING DATE: 2003-02-28
 ; PRIOR APPLICATION NUMBER: US 60/360,039
 ; PRIOR FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 47374
 ; SEQ ID NO 5735
 ; LENGTH: 366
 ; TYPE: PRT
 ; ORGANISM: Caenorhabditis elegans
 US-10-369-493-5735

Query Match 52.0%; Score 52; DB 4; Length 366;
 Best Local Similarity 56.2%; Pred. No. 8;
 Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 5 AGAAASESLFISNHAY 20
 :|||||:|:
 Db 351 AAGAAASESLFVAKHSY 366

Search completed: February 10, 2006, 10:44:47
 Job time : 14.0627 secs

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RESULT 2
US-10-793-626-2802
; Sequence 2802, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU34801US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2802
; LENGTH: 277
; TYPE: prt
; ORGANISM: Artificial Sequence

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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2802

Query Match 42.0%; Score 42; DB 6; Length 277;
Best Local Similarity 47.1%; Pred. No. 7.5; Mismatches 2; Indels 7; Gaps 0;
Matches 8; Conservative 2; Mismatches 2; Indels 7; Gaps 0;

QY 2 SQGAGAAASESLFISNH 18
DB 71 AGDASAIIVSCFVENH 87

RESULT 3

US-10-793-626-3106
; Sequence 3106, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PUS480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3106
; LENGTH: 1027
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-3106

Query Match 42.0%; Score 42; DB 6; Length 1027;
Best Local Similarity 47.1%; Pred. No. 33; Mismatches 2; Indels 7; Gaps 0;
Matches 8; Conservative 2; Mismatches 2; Indels 7; Gaps 0;

QY 2 SQGAGAAASESLFISNH 18
DB 71 AGDASAIIVSCFVENH 87

RESULT 4

US-10-821-234-888
; Sequence 888, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 888
; LENGTH: 748
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-888

Query Match 40.0%; Score 40; DB 6; Length 748;
Best Local Similarity 47.4%; Pred. No. 50; Mismatches 4; Indels 6; Gaps 0;
Matches 9; Conservative 4; Mismatches 4; Indels 6; Gaps 0;

QY 1 PSQAGAAASESLFISNHA 19
DB 653 PSERSGPAASESHRSRHS 671

RESULT 5

US-10-467-657-6628
; Sequence 6628, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6628
; LENGTH: 633
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6628

Query Match 39.0%; Score 39; DB 6; Length 633;
Best Local Similarity 50.0%; Pred. No. 61; Mismatches 7; Indels 3; Gaps 0;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 7 AAASESLFISNHAY 20
DB 186 AIPARTVFIDHAY 199

RESULT 6

US-11-115-639-37
; Sequence 37, Application US/11115639
; Publication No. US20050282242A1
; GENERAL INFORMATION:
; APPLICANT: Rothstein, David
; APPLICANT: Murphy, Christopher
; APPLICANT: MacNeil, Ian
; TITLE OF INVENTION: SCREENING ASSAYS FOR ANTIMICROBIAL
; FILE REFERENCE: 50150/075003
; CURRENT APPLICATION NUMBER: US/11/115,639
; CURRENT FILING DATE: 2005-04-27
; PRIOR APPLICATION NUMBER: 60/566,858
; PRIOR FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: 60/565,679
; PRIOR FILING DATE: 2004-04-27
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 1343
; TYPE: PRT
; ORGANISM: H. influenzae
US-11-115-639-37

Query Match 38.5%; Score 38.5; DB 7; Length 1343;
Best Local Similarity 47.8%; Pred. No. 1.8e+02; Mismatches 11; Indels 3; Gaps 2;
Matches 11; Conservative 3; Mismatches 6; Indels 3; Gaps 2;

QY 1 PSQAGAAASESLF--ISNHAY 20
DB 43 PEGQOGLAARFSPVPIVSNNGY 65

RESULT 7

RESULT 9
US-11-115-639-40
; Sequence 40, Application US/11115639
; Publication No. US20050282242A1
; GENERAL INFORMATION:
; APPLICANT: Rothstein, David

```

RESULT 11
US-11-055-822-88
; Sequence 88, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Habethauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING

```


; TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
 ; FILE REFERENCE: BGI-121CPCN
 ; CURRENT APPLICATION NUMBER: US/11/055,822
 ; CURRENT FILING DATE: 2005-02-11
 ; PRIOR APPLICATION NUMBER: 09/606,740
 ; PRIOR FILING DATE: 2000-06-23
 ; PRIOR APPLICATION NUMBER: 60/141,031
 ; PRIOR FILING DATE: 1999-06-25
 ; PRIOR APPLICATION NUMBER: 60/142,101
 ; PRIOR FILING DATE: 1999-07-02
 ; PRIOR APPLICATION NUMBER: 60/148,613
 ; PRIOR FILING DATE: 1999-08-12
 ; PRIOR APPLICATION NUMBER: 60/187,970
 ; PRIOR FILING DATE: 2000-03-09
 ; PRIOR APPLICATION NUMBER: DE 19930476.9
 ; PRIOR FILING DATE: 1999-07-01
 ; PRIOR APPLICATION NUMBER: DE 19931415.2
 ; PRIOR FILING DATE: 1999-07-08
 ; PRIOR APPLICATION NUMBER: DE 19931418.7
 ; PRIOR FILING DATE: 1999-07-08
 ; PRIOR APPLICATION NUMBER: DE 19931419.5
 ; PRIOR FILING DATE: 1999-07-08
 ; PRIOR APPLICATION NUMBER: DE 19931420.9
 ; PRIOR FILING DATE: 1999-07-08
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 1158
 ; SEQ ID NO 88
 ; LENGTH: 209
 ; TYPE: PRT
 ; ORGANISM: Corynebacterium glutamicum
 ; US-11-055-822-88

Query Match 38.0%; Score 38; DB 7; Length 209;
 Best Local Similarity 44.4%; Pred. No. 26;
 Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2 SQGAGAAASELSFISNHA 19
 |||||::|:|:
 Db 41 SGPAGLAAQAQLTRAGHS 58

RESULT 12
 US-11-055-822-90
 ; Sequence 90, Application US/11055822
 ; Publication No. US20050260707A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pompejus, Markus
 ; APPLICANT: Kroger, Burkhard
 ; APPLICANT: Schroder, Hartwig
 ; APPLICANT: Zelder, Oskar
 ; APPLICANT: Haberhauser, Gregor
 ; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
 ; TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
 ; FILE REFERENCE: BGI-121CPCN
 ; CURRENT APPLICATION NUMBER: US/11/055,822
 ; CURRENT FILING DATE: 2005-02-11
 ; PRIOR APPLICATION NUMBER: 09/606,740
 ; PRIOR FILING DATE: 2000-06-23
 ; PRIOR APPLICATION NUMBER: 60/141,031
 ; PRIOR FILING DATE: 1999-06-25
 ; PRIOR APPLICATION NUMBER: 60/142,101
 ; PRIOR FILING DATE: 1999-07-02
 ; PRIOR APPLICATION NUMBER: 60/148,613
 ; PRIOR FILING DATE: 1999-08-12
 ; PRIOR APPLICATION NUMBER: 60/187,970
 ; PRIOR FILING DATE: 2000-03-09
 ; PRIOR APPLICATION NUMBER: DE 19930476.9
 ; PRIOR FILING DATE: 1999-07-01
 ; PRIOR APPLICATION NUMBER: DE 19931415.2
 ; PRIOR FILING DATE: 1999-07-08
 ; PRIOR APPLICATION NUMBER: DE 19931418.7
 ; PRIOR FILING DATE: 1999-07-08
 ; PRIOR APPLICATION NUMBER: DE 19931419.5

QY 2 SQGAGAAASELSFISNHA 19
 |||||::|:|:
 Db 41 SGPAGLAAQAQLTRAGHS 58

RESULT 13
 US-10-793-626-2868
 ; Sequence 2868, Application US/10793626
 ; Publication No. US2005025478A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KIMMERLY, WILLIAM JOHN
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
 ; FILE REFERENCE: PU3480US
 ; CURRENT APPLICATION NUMBER: US/10/793,626
 ; CURRENT FILING DATE: 2004-03-04
 ; PRIOR APPLICATION NUMBER: 60/164,258
 ; PRIOR FILING DATE: 1999-11-09
 ; NUMBER OF SEQ ID NOS: 4472
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2868
 ; LENGTH: 338
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic
 ; OTHER INFORMATION: amino acid sequence
 ; US-10-793-626-2868

Query Match 38.0%; Score 38; DB 6; Length 338;
 Best Local Similarity 40.0%; Pred. No. 44;
 Matches 8; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY 1 PSQAGAAASELSFISNHAY 20
 |||||::|:|:
 Db 295 PYGASGAALVTRLFYMKHQF 314

RESULT 14
 US-10-517-939-284
 ; Sequence 284, Application US/10517939
 ; Publication No. US20060003433A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Steer, Brian
 ; APPLICANT: Callen, Walter
 ; APPLICANT: Healey, Shaun
 ; APPLICANT: Hazlewood, Geoff
 ; APPLICANT: Wu, Di
 ; APPLICANT: Blum, David
 ; APPLICANT: Esteghlalian, Alireza
 ; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
 ; TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
 ; FILE REFERENCE: 56462007901
 ; CURRENT APPLICATION NUMBER: US/10/517,939
 ; CURRENT FILING DATE: 2004-12-13
 ; PRIOR APPLICATION NUMBER: PCT/US03/19153
 ; PRIOR FILING DATE: 2003-06-16
 ; PRIOR APPLICATION NUMBER: 60/389,299
 ; PRIOR FILING DATE: 2002-06-14

; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 284
; LENGTH: 1386
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Obtained from an environmental sample.
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)....(28)
US-10-517-939-284

Query Match 38.0%; Score 38; DB 6; Length 1386;
Best Local Similarity 44.4%; Pred. No. 2.2e+02;
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2 SQAGAAASESLFISNHA 19
DB 211 SGFEGRAGTETLTVTNEA 228

RESULT 15
US-11-024-959-455
; Sequence 455, Application US/11024959
; Publication No. US20060010516A1
; GENERAL INFORMATION:
; APPLICANT: FORSTER, RICHARD L.
; APPLICANT: CONNETT, MARIE B.
; APPLICANT: EMERSON, SARAH JANE
; APPLICANT: GRIGOR, MURRAY ROBERT
; APPLICANT: HIGGINS, COLLEEN M.
; APPLICANT: LUND, STEVEN TROY
; APPLICANT: MAGUSIN, ANDREAS
; APPLICANT: KODRZYCKI, BOB
; TITLE OF INVENTION: CELL CYCLE GENES AND RELATED METHODS
; FILE REFERENCE: 044463-0360
; CURRENT APPLICATION NUMBER: US/11/024,959
; CURRENT FILING DATE: 2004-12-30
; PRIOR APPLICATION NUMBER: 60/533,036
; PRIOR FILING DATE: 2003-12-30
; NUMBER OF SEQ ID NOS: 782
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 455
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Pinus radiata
US-11-024-959-455

Query Match 37.0%; Score 37; DB 7; Length 327;
Best Local Similarity 69.2%; Pred. No. 63;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 QGAGAAASESLFI 15
DB 258 GQYIASASEDLFI 270

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OM nucleic - nucleic search, using sw model

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Perfect score: 28
Sequence: 1 CACATGTAAACAGACTTCATTTGGC 28

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Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

Database : GenEmbl.*
1: gb_ba.*
2: gb_in.*
3: gb_env.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pr.*
9: gb_ro.*
10: gb_sts.*
11: gb_sy.*
12: gb_un.*
13: gb_vi.*
14: gb_hg.*
15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	28	100.0	28	6 AR003767	AR003767 Sequence
2	28	100.0	28	6 AR010103	AR010103 Sequence
3	28	100.0	28	6 AR055309	AR055309 Sequence
4	28	100.0	28	6 AR141238	AR141238 Sequence
5	28	100.0	28	6 AR141475	AR141475 Sequence
6	28	100.0	28	6 I11949	I11949 Sequence 61
7	28	100.0	28	6 I40520	I40520 Sequence 59
8	28	100.0	28	6 AR368004	AR368004 Sequence
9	28	100.0	28	6 AR430985	AR430985 Sequence
10	24.8	88.6	813	6 AR003721	AR003721 Sequence
11	24.8	88.6	813	6 AR010057	AR010057 Sequence
12	24.8	88.6	813	6 AR055263	AR055263 Sequence
13	24.8	88.6	813	6 AR067747	AR067747 Sequence
14	24.8	88.6	813	6 AR141192	AR141192 Sequence
15	24.8	88.6	813	6 AR141429	AR141429 Sequence
16	24.8	88.6	813	6 AR164985	AR164985 Sequence
17	24.8	88.6	813	6 I11901	I11901 Sequence 11
18	24.8	88.6	813	6 I11947	I11947 Sequence 57

19	24.8	88.6	813	6 I40474	I40474 Sequence 11
20	24.8	88.6	813	6 AR367958	AR367958 Sequence
21	24.8	88.6	813	6 AR430939	AR430939 Sequence
22	24.8	88.6	955	6 AR067753	AR067753 Sequence
23	24.8	88.6	955	6 AR164991	AR164991 Sequence
24	24.8	88.6	1003	6 AR067750	AR067750 Sequence
25	24.8	88.6	1003	6 AR164988	AR164988 Sequence
26	24.8	88.6	1072	6 AR067749	AR067749 Sequence
27	24.8	88.6	1072	6 AR164987	AR164987 Sequence
28	24.8	88.6	1176	15 GLNGELONIN	LI2243 Geloninum mu
29	22.2	79.3	251066	14 AC098147	AC098147 Rattus no
30	22.2	79.3	251066	14 AC118400	AC118400 Rattus no
31	21.8	77.9	533	10 BV319457	BV319457 S236P6160
32	21.8	77.9	110000	1 BX571856_25	Continuation (26 o
33	21.6	77.1	150467	8 AC009541	AC009541 Human Chr
34	21.6	77.1	172237	8 AC083869	AC083869 Homo sapi
35	21.6	77.1	174775	5 BX284691	BX284691 Zebrafish
36	21.2	75.7	121343	14 AC150705	AC150705 Medicago
37	21.2	75.7	123395	14 AC149582	AC149582 Medicago
38	21.2	75.7	245377	14 AC095875	AC095875 Rattus no
39	21.2	75.7	262166	14 AC160493	AC160493 Bos tauru
40	21.2	75.7	288636	14 AC130903	AC130903 Rattus no
41	21.2	75.7	293867	14 AC130587	AC130587 Rattus no
42	20.8	74.3	714	10 PM4B2G	PM4B2G01 Penicilli
43	20.8	74.3	147595	14 AC162139	AC162139 Loxodonta
44	20.8	74.3	153572	5 BX323992	BX323992 Zebrafish
45	20.8	74.3	168773	9 AL731820	AL731820 Mouse DNA

ALIGNMENTS

RESULT 1
AR003767
LOCUS AR003767 28 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 59 from patent US 5744580.
ACCESSION AR003767
VERSION AR003767.1 GI:3965026
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS Better,M.D., Carroll,S.F. and Studnicka,G.M.
TITLE Immunotoxins comprising ribosome-inactivating proteins
JOURNAL Patent: US 5744580-A 59 28-APR-1998;
FEATURES
source
1..28
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 28; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CACATGTAAACAGACTTCATTTGGC 28
|||||
Db 1 CACATGTAAACAGACTTCATTTGGC 28

RESULT 2
AR010103
LOCUS AR010103 28 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 59 from patent US 5756699.
ACCESSION AR010103
VERSION AR010103.1 GI:3969808
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS Better,M.D., Carroll,S.F. and Studnicka,G.M.

TITLE Immunotoxins comprising ribosome-inactivating proteins
JOURNAL Patent: US 5756699-A 59 26-MAY-1998;
FEATURES Location/Qualifiers
source

ORIGIN /organism="unknown"
/mol_type="unassigned DNA"

Query Match 100.0%; Score 28; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CACATGTAACAAGACTTCATTGGC 28
|||||
Db 1 CACATGTAACAAGACTTCATTGGC 28

RESULT 3
LOCUS AR055309 28 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 59 from patent US 5837491.
ACCESSION AR055309
VERSION AR055309.1 GI:5980886
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 28)
AUTHORS Better,M.D., Carroll,S.F. and Studnicka,G.M.
TITLE Polynucleotides encoding gelonin sequences
JOURNAL Patent: US 5837491-A 59 17-NOV-1998;
FEATURES Location/Qualifiers
source

ORIGIN /organism="unknown"
/mol_type="unassigned DNA"

Query Match 100.0%; Score 28; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CACATGTAACAAGACTTCATTGGC 28
|||||
Db 1 CACATGTAACAAGACTTCATTGGC 28

RESULT 4
LOCUS AR141238 28 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 59 from patent US 6146631.
ACCESSION AR141238
VERSION AR141238.1 GI:15100755
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 28)
AUTHORS Better,M.D., Carroll,S.F. and Studnicka,G.M.
TITLE Immunotoxins comprising ribosome-inactivating proteins
JOURNAL Patent: US 6146631-A 59 14-NOV-2000;
FEATURES Location/Qualifiers
source

ORIGIN /organism="unknown"
/mol_type="unassigned DNA"

Query Match 100.0%; Score 28; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CACATGTAACAAGACTTCATTGGC 28
|||||
Db 1 CACATGTAACAAGACTTCATTGGC 28

RESULT 5
LOCUS AR141475 28 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 59 from patent US 6146850.
ACCESSION AR141475
VERSION AR141475.1 GI:15100991
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 28)
AUTHORS Better,M.D. and Carroll,S.F.
TITLE Proteins encoding gelonin sequences
JOURNAL Patent: US 6146850-A 59 14-NOV-2000;
FEATURES Location/Qualifiers
source

ORIGIN /organism="unknown"
/mol_type="unassigned DNA"

Query Match 100.0%; Score 28; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CACATGTAACAAGACTTCATTGGC 28
|||||
Db 1 CACATGTAACAAGACTTCATTGGC 28

RESULT 6
LOCUS I11949 28 bp DNA linear PAT 26-JUL-1995
DEFINITION Sequence 61 from Patent US 5416202.
ACCESSION I11949
VERSION I11949.1 GI:909392
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 28)
AUTHORS Bernhard,S.L., Better,M.D., Carroll,S.F., Lane,J.A. and Lei,S.-P.
TITLE Materials comprising and methods of preparation and use for
ribosome-inactivating proteins
JOURNAL Patent: US 5416202-A 61 16-MAY-1995;
FEATURES Location/Qualifiers
source

ORIGIN /organism="unknown"
/mol_type="unassigned DNA"

Query Match 100.0%; Score 28; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CACATGTAACAAGACTTCATTGGC 28
|||||
Db 1 CACATGTAACAAGACTTCATTGGC 28

RESULT 7
LOCUS I40520 28 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 59 from patent US 5621083.
ACCESSION I40520
VERSION I40520.1 GI:2082812
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 28)
AUTHORS Better,M.D., Carroll,S.F. and Studnicka,G.M.

TITLE Immunotoxins comprising ribosome-inactivating proteins
JOURNAL Patent: US 5621083-A 59 15-APR-1997;
FEATURES Location/Qualifiers
source 1..28
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 28; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CACATGTAATAACAAGACTTCATTTTGGC 28
Db 1 CACATGTAATAACAAGACTTCATTTTGGC 28

RESULT 8
AR368004
LOCUS AR368004 28 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 59 from patent US 6376217.
ACCESSION AR368004
VERSION AR368004.1 GI:34601515
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 28)
AUTHORS Better,M.D. and Carroll,S.F.
TITLE Fusion proteins and polynucleotides encoding gelonin sequences
JOURNAL Patent: US 6376217-A 59 23-APR-2002;
Xoma Technology Ltd.;;
BMX;
FEATURES Location/Qualifiers
source 1..28
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 28; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CACATGTAATAACAAGACTTCATTTTGGC 28
Db 1 CACATGTAATAACAAGACTTCATTTTGGC 28

RESULT 9
AR430985
LOCUS AR430985 28 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 59 from patent US 6649742.
ACCESSION AR430985
VERSION AR430985.1 GI:40192816
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 28)
AUTHORS Better,M.D., Carroll,S.F. and Studnicka,G.M.
TITLE Immunotoxins comprising ribosome-inactivating proteins
JOURNAL Patent: US 6649742-A 59 18-NOV-2003;
XOMA Technology Ltd.;;
BEX;
FEATURES Location/Qualifiers
source 1..28
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 28; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CACATGTAATAACAAGACTTCATTTTGGC 28
Db 1 CACATGTAATAACAAGACTTCATTTTGGC 28

RESULT 10

AR003721
LOCUS AR003721 813 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 11 from patent US 5744580.
ACCESSION AR003721
VERSION AR003721.1 GI:3964980
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 813)
AUTHORS Better,M.D., Carroll,S.F. and Studnicka,G.M.
TITLE Immunotoxins comprising ribosome-inactivating proteins
JOURNAL Patent: US 5744580-A 11 28-APR-1998;
FEATURES Location/Qualifiers
source 1..813
/organism="unknown"
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ORIGIN

Query Match 88.6%; Score 24.8; DB 6; Length 813;
Best Local Similarity 92.9%; Pred. No. 14;
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 CACATGTAATAACAAGACTTCATTTTGGC 28
Db 303 CACAATTAAACAAGACTTCATTTTGGC 330

RESULT 11

AR010057
LOCUS AR010057 813 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 11 from patent US 5756699.
ACCESSION AR010057
VERSION AR010057.1 GI:3968862
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 813)
AUTHORS Better,M.D., Carroll,S.F. and Studnicka,G.M.
TITLE Immunotoxins comprising ribosome-inactivating proteins
JOURNAL Patent: US 5756699-A 11 26-MAY-1998;
FEATURES Location/Qualifiers
source 1..813
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 88.6%; Score 24.8; DB 6; Length 813;
Best Local Similarity 92.9%; Pred. No. 14;
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 CACATGTAATAACAAGACTTCATTTTGGC 28
Db 303 CACAATTAAACAAGACTTCATTTTGGC 330

RESULT 12

AR055263
LOCUS AR055263 813 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 11 from patent US 5837491.
ACCESSION AR055263
VERSION AR055263.1 GI:5980840
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

Unclassified.									
REFERENCE	1 (bases 1 to 813)								
AUTHORS	Better,M.D., Carroll,S.F. and Studnicka,G.M.								
TITLE	Polynucleotides encoding gelonin sequences								
JOURNAL	Patent: US 5837491-A 11 17-NOV-1998;								
FEATURES	Location/Qualifiers								
source	1..813								
	/organism="unknown"								
	/mol_type="unassigned DNA"								
ORIGIN									
Query Match	88.6%; Score 24.8; DB 6; Length 813;								
Best Local Similarity	92.9%; Pred. No. 14;								
Matches	26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;								
QY	1 CACATGTAATAAACAGACTTCATTATTGGC 28								
DB	303 CACAAATTAATAACAGACTTCATTATTGGC 330								
RESULT 13									
AR067747	AR067747 813 bp DNA linear PAT 29-SEP-1999								
LOCUS	Sequence 246 from patent US 5851802.								
DEFINITION	AR067747								
ACCESSION	AR067747.1 GI:5998969								
VERSION	.								
KEYWORDS	Unknown.								
SOURCE	Unknown.								
ORGANISM	Unclassified.								
REFERENCE	1 (bases 1 to 813)								
AUTHORS	Better,M.D.								
TITLE	Methods for recombinant microbial production of fusion proteins and BPI-derived peptides								
JOURNAL	Patent: US 5851802-A 246 22-DEC-1998;								
FEATURES	Location/Qualifiers								
source	1..813								
	/organism="unknown"								
	/mol_type="unassigned DNA"								
ORIGIN									
Query Match	88.6%; Score 24.8; DB 6; Length 813;								
Best Local Similarity	92.9%; Pred. No. 14;								
Matches	26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;								
QY	1 CACATGTAATAAACAGACTTCATTATTGGC 28								
DB	303 CACAAATTAATAACAGACTTCATTATTGGC 330								
RESULT 14									
AR141192	AR141192 813 bp DNA linear PAT 08-AUG-2001								
LOCUS	Sequence 11 from patent US 6146631.								
DEFINITION	AR141192								
ACCESSION	AR141192.1 GI:15100709								
VERSION	.								
KEYWORDS	Unknown.								
SOURCE	Unknown.								
ORGANISM	Unclassified.								
REFERENCE	1 (bases 1 to 813)								
AUTHORS	Better,M.D., Carroll,S.F. and Studnicka,G.M.								
TITLE	Immunotoxins comprising ribosome-inactivating proteins								
JOURNAL	Patent: US 6146631-A 11 14-NOV-2000;								
FEATURES	Location/Qualifiers								
source	1..813								
	/organism="unknown"								
	/mol_type="unassigned DNA"								
ORIGIN									
Query Match	88.6%; Score 24.8; DB 6; Length 813;								
Best Local Similarity	92.9%; Pred. No. 14;								
Matches	26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;								

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 12, 2006, 23:16:37 ; Search time 271 Seconds
(without alignments)
688.603 Million cell updates/sec

Title: US-10-717-243-59

Perfect score: 28

Sequence: 1 CACATGTAAACAAAGACTTCATTTGGC 28

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: Geneseqn1980s.*

2: Geneseqn1990s.*

3: Geneseqn2000s.*

4: Geneseqn2001as.*

5: Geneseqn2001bs.*

6: Geneseqn2002as.*

7: Geneseqn2002bs.*

8: Geneseqn2003as.*

9: Geneseqn2003bs.*

10: Geneseqn2003cs.*

11: Geneseqn2003ds.*

12: Geneseqn2004as.*

13: Geneseqn2004bs.*

14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	100.0	28	2	AAQ42253 PCR prime
2	24.8	88.6	813	2	AAQ48031 Encodes p
3	24.8	88.6	813	2	AAQ42222 Encodes p
4	24.8	88.6	813	2	AAQ75532 Type I ri
5	24.8	88.6	813	2	AAQ92342 Type I ri
6	24.8	88.6	955	2	AAQ86336 BPI pepti
7	24.8	88.6	1003	2	AAQ86341 BPI pepti
8	24.8	88.6	1072	2	AAQ86332 BPI pepti
9	24.8	88.6	1176	6	AB556021 cDNA enco
10	24.8	88.6	1500	14	AB568721 scFv23-ge
11	24.8	88.6	1527	6	AB556029 DNA encod
12	20.6	73.6	38142	13	ABD32682 Mouse can
13	20.2	72.1	2103	8	ACF73271 Staphyloc
14	20.2	72.1	2187	2	AAV74640 Staphyloc
15	20	71.4	11298	2	AA867556 Human hlg
16	20	71.4	11298	2	AAV54661 Human bet
17	20	71.4	11298	3	AA34815 Human ade
18	20	71.4	11298	3	AAQ20937 Human hlg
19	20	71.4	11298	4	AAQ92144 Human IGE

20	20	71.4	11298	10	ABZ96631 Human hlg
21	20	71.4	11298	11	ABD19056 Human hlg
22	20	71.4	11357	2	AAQ51024 Human FCE
23	20	71.4	21742	3	AA34816 Human ade
24	20	71.4	21742	3	AAQ20938 Human hlg
25	20	71.4	21742	10	ABZ96632 Human hlg
26	20	71.4	21742	11	ABD19051 Human hlg
27	20	71.4	33030	5	AAQ29337 Atopy rel
28	20	71.4	117608	10	ABZ97129 Human rec
29	20	71.4	117609	3	AAQ21435 Human rec
30	20	71.4	117609	11	ABD17968 Human rec
c 31	19.8	70.7	1637	6	AAQ43749 Human AGT
c 32	19.8	70.7	2361	6	AAQ43751 Human AGT
c 33	19.8	70.7	2361	6	AAQ43821 Human AGT
34	19.8	70.7	4102	6	AAQ18667 Reference
35	19.8	70.7	4788	2	AAQ85367 MIP-1-1p
36	19.6	70.0	2949	8	ACF03675 Human eph
37	19.6	70.0	2953	6	ABV78119 Human eph
38	19.6	70.0	2953	6	ABZ35695 Human eph
39	19.6	70.0	2953	6	ABX09938 Human eph
40	19.6	70.0	2953	6	ABL91660 Human pol
41	19.6	70.0	3132	2	AAQ34513 HEK codin
42	19.6	70.0	3149	3	AA64458 CDNA enco
43	19.6	70.0	3149	8	ABZ34862 Coding se
44	19.6	70.0	3149	10	AAQ58484 Human rec
45	19.6	70.0	3149	10	ABD75272 Prostate

ALIGNMENTS

RESULT 1

ID AAQ42253 standard; cDNA; 28 BP.

AC AAQ42253;

DT 25-MAR-2003 (revised)

DT 13-SEP-1993 (first entry)

DE PCR primer Geloc-20 to replace Ile103 of gelonin with Cys.

XX Type I ribosome-inactivating protein; ricin; momordin; immunoconjugate;
XX autoimmune disease; cell killing; toxin;
XX Mutagenic polymerase chain reaction; ss.

OS Synthetic.

XX WO9309130-A1.

PD 13-MAY-1993.

PF 04-NOV-1992; 92WO-US009487.

PR 04-NOV-1991; 91US-00787567.

XX 19-JUN-1992; 92US-00901707.

XX (XOMA) XOMA CORP.

PI Bernhard SL, Better MD, Carroll SF, Lane JA, Lei SP;

XX WPI; 1993-167617/20.

PT Analogues of type I ribosome inactivating protein - useful as cytotoxic
PT agents, immuno toxins for treating autoimmune diseases, cancer, graft
PT versus host disease and selective cell killing in vivo.

XX Example 3; Page 35; 163pp; English.

CC Fifteen analogues of gelonin were constructed. Ten non-cysteine residues
CC in surface positions and available for conjugation to a second protein
CC were targeted for substn. In the other analogues, one or both of the
CC native Cys residues present in gelonin were substd. Overlap extension PCR

CC was used to construct the various analogues. Primer geloC-20 was used in
 CC the subseq. of Ile103 of gelonin by Cys. (Updated on 25-MAR-2003 to
 CC correct PN field.)

SQ Sequence 28 BP; 10 A; 6 C; 4 G; 8 T; 0 U; 0 Other;
 Query Match 100.0%; Score 28; DB 2; Length 28;
 Best Local Similarity 100.0%; Pred. No. 0.051; 0; Indels 0; Gaps 0;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACATGTAACAAGACTTCATTGGC 28
 |||||
 Db 1 CACATGTAACAAGACTTCATTGGC 28

RESULT 2
 ID AAQ48031 standard; cDNA; 813 BP.

XX AC AAQ48031;

XX 25-MAR-2003 (revised)
 DT 13-SEP-1993 (first entry)

DE Encodes plant type I RIP Gelonin.

XX Type I ribosome-inactivating protein; ricin; immunoconjugate;
 KW autoimmune disease; cell killing; toxin; Euphorbiaceae family.

XX Gelonium multiflorum.

XX WO9309130-A1.

XX 13-MAY-1993.

XX 04-NOV-1992; 92WO-US009487.

XX 04-NOV-1991; 91US-00787567.

XX 19-JUN-1992; 92US-00901707.

XX (XOMA) XOMA CORP.

XX Berhard SL, Better MD, Carroll SF, Lane JA, Lei SP;

XX WPI; 1993-167617/20.

XX Analogues of type I ribosome inactivating protein - useful as cytotoxic
 PT agents, immuno toxins for treating autoimmune diseases, cancer, graft
 PT versus host disease and selective cell killing in-vivo.

XX Claim 85; Page 114; 163pp; English.

XX The invention covers analogues of Type I RIPs. Gelonin is a Type I RIP
 CC and the analogues of the invention have a cysteine available for
 CC intermolecular disulphide bonding at an amino acid position corresp. to a
 CC position not naturally available for bonding; the cys residue is located
 CC in the C-terminal region of the analogue between a position corresp. to
 CC amino acid 251 and the C-terminus of ricin A chain. The analogues are
 CC pref. joined via a disulphide linkage to a molecule which specifically
 CC binds to a target cell, e.g. an antibody fragment. See AAR37291 for
 CC gelonin amino acid sequence. (Updated on 25-MAR-2003 to correct PN
 CC field.)

SQ Sequence 813 BP; 266 A; 150 C; 182 G; 215 T; 0 U; 0 Other;

Query Match 88.6%; Score 24.8; DB 2; Length 813;
 Best Local Similarity 92.9%; Pred. No. 1.6;
 Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CACATGTAACAAGACTTCATTGGC 28
 |||||
 Db 303 CACATTAACAAGACTTCATTGGC 330

RESULT 3
 ID AAQ42222 standard; cDNA; 813 BP.

XX AC AAQ42222;

XX 25-MAR-2003 (revised)

DT 13-SEP-1993 (first entry)

XX Encodes plant type I RIP Gelonin.

XX Type I ribosome-inactivating protein; ricin; momordin; immunoconjugate;
 KW autoimmune disease; cell killing; toxin; Euphorbiaceae family; ss.

XX Gelonium multiflorum.

XX WO9309130-A1.

XX 13-MAY-1993.

XX 04-NOV-1992; 92WO-US009487.

XX 04-NOV-1991; 91US-00787567.

XX 19-JUN-1992; 92US-00901707.

XX (XOMA) XOMA CORP.

XX Berhard SL, Better MD, Carroll SF, Lane JA, Lei SP;

XX WPI; 1993-167617/20.

XX Analogues of type I ribosome inactivating protein - useful as cytotoxic
 PT agents, immuno toxins for treating autoimmune diseases, cancer, graft
 PT versus host disease and selective cell killing in-vivo.

XX Claim 85; Page 101; 163pp; English.

XX Proteolytic peptide fragments of native gelonin were sequenced. PCR
 CC primers were designed based on these peptide fragments. The primers were
 CC used to amplify segments of cDNA covering the 5'-terminal, middle and 3'-
 CC terminal regions of the gelonin coding sequence. A composite gelonin gene
 CC sequence was assembled from the overlapping gelonin DNA fragments (see
 CC AAQ42222). Having cloned the gelonin gene, the development of gelonin
 CC analogues and gene fusions is facilitated. See AAR37291 for gelonin amino
 CC acid sequence. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 813 BP; 267 A; 150 C; 180 G; 216 T; 0 U; 0 Other;

Query Match 88.6%; Score 24.8; DB 2; Length 813;
 Best Local Similarity 92.9%; Pred. No. 1.6;
 Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CACATGTAACAAGACTTCATTGGC 28
 |||||

Db 303 CACATTAACAAGACTTCATTGGC 330

RESULT 4
 ID AAQ75532 standard; cDNA; 813 BP.

XX AC AAQ75532;

XX 25-MAR-2003 (revised)

DT 27-JUL-1995 (first entry)

XX Type I ribosome-inactivating protein gelonin cDNA.

XX Type I ribosome-inactivating proteins; RIPs; gelonin;
 KW cytotoxic therapeutic agents; autoimmune disease; cancer;
 KW graft-versus-host disease; ss.


```

OS Gelonium multiflorum.
XX
XX Key Location/Qualifiers
XX mat_peptide 1..810
XX /tag= a
XX /transl_except= pos:754..810
XX /note= "no corresponding amino acids"
XX
XX WO9426910-A1.
XX
XX 24-NOV-1994.
XX
XX 12-MAY-1994; 94WO-US005348.
XX
XX 12-MAY-1993; 93US-00064691.
XX
XX (XOMA ) XOMA CORP.
XX
XX Better MD, Carroll SF, Studnicka GM;
XX
XX WPI; 1995-006804/01.
XX P-PSDB; AAR63903.
XX
XX Polynucleotide(s) encoding type I ribosome-inactivating proteins - which
XX are suitable for use as components of cytotoxic therapeutic agents.
XX
XX Example 1; Page 155; 22ipp; English.
XX
XX AAQ75532 encodes AAR63903 type I ribosome-inactivating protein (RIP)
XX gelonin, one of the nine RIPs described in AAR63903-R63911. RIPs are key
XX components of cytotoxic therapeutic agents (CTAs), which include gene
XX fusion products and immunoconjugates. CTAs may be used to selectively
XX eliminate any cell type to which a RIP component is targeted, by the
XX specific binding capacity of the second component of the agent. They can
XX be used in the treatment of diseases where the elimination of a
XX particular cell type is desired, such as autoimmune disease, cancer and
XX graft-versus-host disease. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 813 BP; 267 A; 150 C; 180 G; 216 T; 0 U; 0 Other;

Query Match 88.6%; Score 24.8; DB 2; Length 813;
Best Local Similarity 92.9%; Pred. No. 1.6;
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CACATGTAAACAAGACTTCATTTTGGC 28
DB 303 CACAATTAAACAAGACTTCATTTTGGC 330

RESULT 5
AAQ92342
ID AAQ92342 standard; DNA; 813 BP.
XX
XX AC AAQ92342;
XX
XX 25-MAR-2003 (revised)
XX 01-JAN-1996 (first entry)
XX
XX Type I ribosome-inactivating protein gelonin gene.
XX
XX Ribosome inactivating protein; RIP; Type I; cytotoxin; immunotoxin; ss.
XX Gelonium multiflorum.
XX
XX US5416202-A.
XX
XX 16-MAY-1995.
XX
XX 09-DEC-1992; 92US-00988430.
XX
XX 04-NOV-1991; 91US-00787567.
XX 19-JUN-1992; 92US-00901707.
XX

```

```

PA (XOMA ) XOMA CORP.
XX
XX Lei S, Carroll SF, Lane JA, Bernhard SL, Better MD;
XX
XX WPI; 1995-193480/25.
XX
XX Polynucleotide(s) encoding gelonin analogues - having a cysteine residue
XX for intermolecular bonding for the prodn. of immuno-toxin(s).
XX
XX Example; Col 71-72; 66pp; English.
XX
XX Analogues of Type I RIP are defined as non-naturally occurring
XX polypeptides that share the ribosome-inactivating activity of the natural
XX protein but differ in AA sequence. Preferred analogues have a Cys
XX available for disulfide bonding located at a posn. it its AA sequence
XX from the posn. corresp. to posn. 251 in ricin A-chain RTA to the carboxy
XX terminus of the analogue. (AAR74176 is the sequence of ricin A-chain RTA,
XX which is a Type II RIP). The primary AA sequence of the Type I RIPs
XX gelonin, BRIP, mormordin II, luffin [see Islam et al. Agricultural
XX Biological Chem., 54(5) 1343-45 1991], alphatrachosanthin [see Chow et
XX al., J. Biol. Chem., 265, 8670-74 1990], momordin I [see Ho et al., BBA,
XX 1088, 311-14 1991], Mirabilis antiviral protein [see Habuka et al., J.
XX Biol. Chem., 264(12) 6629-37 1989], pokeweed antiviral protein isolated
XX from seeds [see Kung et al., Agric. Biol. Chem., 54(12), 3301-18 1990]
XX and saporin [see Banatti et al., Eur. J. Biochem., 183, 465-70 1989] are
XX individually aligned with the primary sequence of the ricin A-chain [see
XX Halling et al., Nucleic Acids Res., 13, 8019-8033 1985] respectively in
XX Figures 1-9. The AAs invariant among the ricin A-chain and the Type I
XX RIPs are indicated in FT. Also indicated are the preferred sites of Cys
XX substitution. It is also preferred that the gelonin cysteine residues at
XX positions 44 and 50 be replaced with alanine residues. The complete DNA
XX sequence of the gelonin gene is set out in AAQ92342. (Updated on 25-MAR-
XX 2003 to correct PR field.)
XX
XX Sequence 813 BP; 267 A; 150 C; 180 G; 216 T; 0 U; 0 Other;

Query Match 88.6%; Score 24.8; DB 2; Length 813;
Best Local Similarity 92.9%; Pred. No. 1.6;
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CACATGTAAACAAGACTTCATTTTGGC 28
DB 303 CACAATTAAACAAGACTTCATTTTGGC 330

RESULT 6
AAT86336
ID AAT86336 standard; DNA; 955 BP.
XX
XX AC AAT86336;
XX
XX 20-APR-1998 (first entry)
XX
XX BPI peptide fusion protein pING3797 vector construct.
XX
XX Bactericidal/permeability increasing peptide; BPI; fusion protein;
XX bacterial infection; fungal infection; endotoxin; heparin; angiogenesis;
XX fungicidal; recombinant DNA; vector; ss.
XX
XX Synthetic.
XX Pectobacterium carotovorum.
XX Homo sapiens.
XX Chimeric.
XX
XX Key Location/Qualifiers
XX misc_signal 1..22
XX /tag= a
XX /label= pel_B
XX /standard_name= "Leader"
XX /note= "pel B is the leader sequence from the pectate
XX lyase gene of Erwinia carotovora"
XX 23..273
XX misc_feature
XX /tag= b

```



```

FT /label= gelonin
FT /note= "gelonin - see U.S. Patent No. 5,416,202"
FT CDS 66..944
FT /*tag= c
FT misc_feature 274..275
FT /*tag= d
FT /label= EagI
FT /note= "EagI cloning site"
FT misc_feature 276..279
FT /*tag= g
FT /label= cleavage linker
FT /note= "Ala-Leu-Asp-Pro linking sequence with Asp-Pro
FT /label= peptide sequence
FT /note= "BPI-derived peptide"
FT
FT
XX WO9735009-A1.
XX
XX 25-SEP-1997.
XX
XX 18-MAR-1997; 97WO-US005287.
XX
XX 22-MAR-1996; 96US-00621803.
XX
XX (XOMA ) XOMA CORP.
XX
XX Better MD;
XX
XX WPI; 1997-480215/44.
XX P-PSDB; AAW29300.
XX
XX Recombinant production of bactericidal/permeability increasing protein -
XX by expression as a fusion protein in microbial host cells, then cleaving
XX the BPI peptide from the carrier.
XX
XX Example 1; Page 160-161, 186pp; English.
XX
XX A new recombinant DNA vector construct has been developed which encodes a
XX fusion protein and is suitable for introduction into a bacterial host.
XX The vector comprises: (a) DNA encoding at least one cationic
XX bactericidal/permeability increasing peptide (BPI), (b) DNA encoding a
XX carrier protein, and (c) DNA encoding an amino acid (aa) cleavage site
XX located between (a) and (b). The present sequence represents the pING3797
XX vector construct coding for a BPI fusion protein. The peptides have many
XX uses including the treatment of bacterial and fungal infections. BPI
XX peptides also bind to endotoxins and heparin, neutralising their effects.
XX The peptides have further been shown to inhibit angiogenesis (partly due
XX to heparin-binding activity). The fusion proteins have been found to be
XX expressed in large amounts without significant proteolysis, and in some
XX cases are actually secreted from the host cells. This allows the indirect
XX production of anti-microbial BPI peptides in microbial hosts
XX
XX Sequence 955 BP; 307 A; 189 C; 216 G; 243 T; 0 U; 0 Other;
XX
XX Query Match 88.6%; Score 24.8; DB 2; Length 955;
XX Best Local Similarity 92.9%; Pred. No. 1.6;
XX Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1 CACATGTAACCAAGACTTCATTTCGC 28
XX ||| ||||| ||||| ||||| |||||
XX Db 434 CACAATTAACCAAGACTTCATTTCGC 461
XX
XX RESULT 7
XX AAT86341
XX ID AAT86341 standard; DNA; 1003 BP.
XX
XX AAT86341;
XX
XX 20-APR-1998 (first entry)
XX
XX

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```

DE BPI peptide fusion protein pING3795 vector construct.
XX
XX Bactericidal/permeability increasing peptide; BPI; fusion protein;
XX bacterial infection; fungal infection; endotoxin; heparin; angiogenesis;
XX fungicidal; recombinant DNA; vector; ss.
XX
XX Synthetic.
XX Pectobacterium carotovorum.
XX Homo sapiens.
XX Chimeric.
XX
XX Key Location/Qualifiers
XX misc_signal 1..22
XX /*tag= a
XX /label= pel_B
XX /standard_name= "Leader"
XX /note= "pel B is the leader sequence from the pectate
XX lyase gene of Erwinia carotovora"
XX 23..273
XX /*tag= b
XX /label= gelonin
XX /note= "gelonin - see U.S. Patent No. 5,416,202"
XX 66..992
XX /*tag= c
XX 274..275
XX /*tag= d
XX /label= EagI
XX /note= "EagI cloning site"
XX 276..279
XX /*tag= g
XX /label= cleavage linker
XX /note= "Ala-Leu-Asp-Pro linking sequence with Asp-Pro
XX cleavage site"
XX 280..309
XX /*tag= h
XX /label= peptide sequence
XX /note= "BPI-derived peptide"
XX
XX WO9735009-A1.
XX
XX 25-SEP-1997.
XX
XX 18-MAR-1997; 97WO-US005287.
XX
XX 22-MAR-1996; 96US-00621803.
XX
XX (XOMA ) XOMA CORP.
XX
XX Better MD;
XX
XX WPI; 1997-480215/44.
XX P-PSDB; AAW29303.
XX
XX Recombinant production of bactericidal/permeability increasing protein -
XX by expression as a fusion protein in microbial host cells, then cleaving
XX the BPI peptide from the carrier.
XX
XX Example 1; Page 152-153; 186pp; English.
XX
XX A new recombinant DNA vector construct has been developed which encodes a
XX fusion protein and is suitable for introduction into a bacterial host.
XX The vector comprises: (a) DNA encoding at least one cationic
XX bactericidal/permeability increasing peptide (BPI), (b) DNA encoding a
XX carrier protein, and (c) DNA encoding an amino acid (aa) cleavage site
XX located between (a) and (b). The present sequence represents the pING3795
XX vector construct coding for a BPI fusion protein. The peptides have many
XX uses including the treatment of bacterial and fungal infections. BPI
XX peptides also bind to endotoxins and heparin, neutralising their effects.
XX The peptides have further been shown to inhibit angiogenesis (partly due
XX to heparin-binding activity). The fusion proteins have been found to be
XX expressed in large amounts without significant proteolysis, and in some
XX cases are actually secreted from the host cells. This allows the indirect
XX production of anti-microbial BPI peptides in microbial hosts
XX
XX

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XX  Sequence 1003 BP; 325 A; 194 C; 227 G; 257 T; 0 U; 0 Other;
XX  Query Match      88.6%; Score 24.8; DB 2; Length 1003;
XX  Best Local Similarity 92.9%; Pred. No. 1.6;
XX  Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY  1 CACATGTAACAACAGACTTCATTTCGGC 28
DB  434 CACAATTAACAACAGACTTCATTTCGGC 461

RESULT 8
AAT86332
ID  AAT86332 standard; DNA; 1072 BP.
XX
AC  AAT86332;
XX
DT  20-APR-1998 (first entry)
XX
DE  BPI peptide fusion protein pING3793 vector construct.
XX
KW  Bactericidal/permeability increasing peptide; BPI; fusion protein;
KW  bacterial infection; fungal infection; endotoxin; heparin; angiogenesis;
KW  fungicidal; recombinant DNA; vector; ss.
XX
OS  Synthetic.
OS  Pectobacterium carotovorum.
OS  Homo sapiens.
OS  Chimeric.
XX
XX  Key Location/Qualifiers
XX  misc_signal 1..22
XX  /tag= a
XX  /label= pel B
XX  /standard_name= "Leader"
XX  /note= "pel B is the leader sequence from the pectate
XX  lyase gene of Erwinia carotovora"
XX  23..273
XX  misc_feature
XX  /tag= b
XX  /label= gelonin
XX  /note= "gelonin - see U.S. Patent No. 5,416,202"
XX  66..1064
XX  CDS
XX  /tag= c
XX  274..276
XX  misc_feature
XX  /tag= d
XX  /label= EagI
XX  /note= "EagI cloning site"
XX  277..296
XX  misc_feature
XX  /tag= e
XX  /label= SLT linker
XX  /note= "SLT from shiga-like-toxin gene"
XX  297..298
XX  misc_feature
XX  /tag= f
XX  /label= FspI/ScaI
XX  /note= "FspI and ScaI cloning sites"
XX  299..302
XX  misc_feature
XX  /tag= g
XX  /label= cleavage linker
XX  /note= "Ala-Leu-Asp-Pro linking sequence with Asp-Pro
XX  cleavage site"
XX  303..332
XX  misc_feature
XX  /tag= h
XX  /label= peptide sequence
XX  /note= "BPI-derived peptide"
XX
XX  WO9735009-A1.
XX
XX  25-SEP-1997.
XX
XX  18-MAR-1997; 97WO-US005287.
XX
XX  22-MAR-1996; 96US-00621803.
XX

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XX  (XOMA ) XOMA CORP.
XX  Better MD;
XX
XX  WPI: 1997-480215/44.
XX  P-PSDB; AA292294.
XX
XX  Recombinant production of bactericidal/permeability increasing protein -
XX  by expression as a fusion protein in microbial host cells, then cleaving
XX  the BPI peptide from the carrier.
XX
XX  Example 1; Page 148-150; 186pp; English.
XX
XX  A new recombinant DNA vector construct has been developed which encodes a
XX  fusion protein and is suitable for introduction into a bacterial host.
XX  The vector comprises: (a) DNA encoding at least one cationic
XX  bactericidal/permeability increasing peptide (BPI); (b) DNA encoding a
XX  carrier protein, and (c) DNA encoding an amino acid (aa) cleavage site
XX  located between (a) and (b). The present sequence represents the pING3793
XX  vector construct coding for a BPI fusion protein. The peptides have many
XX  uses including the treatment of bacterial and fungal infections. BPI
XX  peptides also bind to endotoxins and heparin, neutralising their effects.
XX  The peptides have further been shown to inhibit angiogenesis (partly due
XX  to heparin-binding activity). The fusion proteins have been found to be
XX  expressed in large amounts without significant proteolysis, and in some
XX  cases are actually secreted from the host cells. This allows the indirect
XX  production of anti-microbial BPI peptides in microbial hosts
XX
XX  Sequence 1072 BP; 340 A; 210 C; 244 G; 278 T; 0 U; 0 Other;
XX
XX  Query Match      88.6%; Score 24.8; DB 2; Length 1072;
XX  Best Local Similarity 92.9%; Pred. No. 1.6;
XX  Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY  1 CACATGTAACAACAGACTTCATTTCGGC 28
DB  434 CACAATTAACAACAGACTTCATTTCGGC 461

RESULT 9
AAT86332
ID  AAT86332 standard; cDNA; 1176 BP.
XX
AC  AAT86332;
XX
DT  08-JAN-2003 (first entry)
XX
DE  cDNA encoding G. multiflorum recombinant gelonin (rGel) toxin.
XX
KW  Modified protein; reduced antigenicity; modified toxin; gelonin;
KW  designer toxin; immunotoxin; proteinaceous compound; cancer;
KW  microbial pathogenesis; acquired immunodeficiency syndrome; AIDS;
KW  autoimmune disease; hyperproliferative disorder; leukaemia; arthritis;
KW  inflammatory disease; cardiovascular disease; diabetes;
KW  pathogenic disease; cytostatic; antiarthritic; antiinflammatory;
KW  cardiant; antidiabetic; virucide; protozoacide; fungicide; antibacterial;
KW  recombinant gelonin; rGel; gene; ss.
XX
XX  Gelonium multiflorum.
XX
XX  Key Location/Qualifiers
XX  CDS
XX  24..974
XX  /tag= a
XX  /product= "rGel"
XX
XX  WO200269886-A2.
XX
XX  12-SEP-2002.
XX
XX  12-FEB-2002; 2002WO-US004195.
XX
XX  12-FEB-2001; 2001US-0268402P.
XX

```


XX (RERE-) RES DEV FOUND.
 XX Rosenblum MG, Cheung L;
 XX WPI; 2002-750431/81.
 XX P-PSDB; ABG71551.
 XX
 XX Generating a modified protein with reduced antigenicity for treating
 XX cancer, AIDS, autoimmune diseases, comprises identifying a protein region
 XX antigenic in the first subject using antiserum from either the first or a
 XX second subject.
 XX
 XX Example 1; Page 170; 176pp; English.
 XX
 XX The present invention relates to a method of generating a modified
 XX protein with reduced antigenicity while maintaining its biological
 XX activity. The method comprises identifying a region of the protein that
 XX is antigenic in a first subject using antiserum from either the first
 XX subject or a second subject of the same species as the first subject. In
 XX particular the invention discloses modified toxin compounds, for example
 XX gelonin toxin derived from Gelonium multiflorum, that are truncated
 XX and/or possess reduced antigenicity. Such designer toxins have
 XX therapeutic, diagnostic, and preventative benefits, particularly as
 XX immunotoxins. The method of the invention is useful for generating
 XX proteinaceous compounds with less antigenicity. The immunotoxin and
 XX gelonin toxin are useful for treating cancer, e.g. prostate, lung, brain,
 XX skin, liver, breast, lymphoid, stomach, testicular, ovarian, pancreatic,
 XX bone, bone marrow, head and neck, cervical, oesophagus, eye, gall
 XX bladder, kidney, adrenal glands, heart, colon, or blood cancer. The
 XX compositions of the invention are also useful for treating microbial
 XX pathogenesis, acquired immunodeficiency syndrome (AIDS), autoimmune
 XX diseases, hyperproliferative disorders including cancer, leukaemia,
 XX arthritis, inflammatory diseases, cardiovascular diseases, pathogenic
 XX diseases, and diabetes. The method provides less antigenic proteins,
 XX peptides and polypeptides, which are more effective than prior art. The
 XX present sequence encodes G. multiflorum recombinant gelonin (rGel)
 XX
 XX Sequence 1176 BP; 369 A; 211 C; 263 G; 333 T; 0 U; 0 Other;
 XX
 XX Query Match 88.6%; Score 24.8; DB 6; Length 1176;
 XX Best Local Similarity 92.9%; Pred. No. 1.6;
 XX Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 XX
 XX QY 1 CACATGTAACAAAGACTTCATTTCGC 28
 XX |||||
 XX Db 464 CACAATTAACAAAGACTTCATTTCGC 491
 XX
 XX RESULT 10
 XX AEB68721
 XX ID AEB68721 standard; DNA; 1500 BP.
 XX AC AEB68721;
 XX
 XX DT 06-OCT-2005 (first entry)
 XX
 XX DE scFv23-gelonin immunotoxin nucleotide sequence SEQ ID NO:12.
 XX
 XX KW antibody engineering; c-erbB-2 protein; toxin; gelonin; cytostatic;
 XX immunotoxin; neoplasm; gene; db.
 XX
 XX OS Synthetic.
 XX
 XX FH Key Location/Qualifiers
 XX FT CDS 1..1497
 XX FT /*tag= a
 XX FT /product= "scFv23-gelonin immunotoxin"
 XX
 XX PN US2005163774-A1.
 XX PD 28-JUL-2005.
 XX

PF 13-OCT-2004; 2004US-00964195.
 XX
 XX PR 10-APR-1992; 92US-00867728.
 XX PR 09-DEC-1993; 93US-00164638.
 XX PR 02-SEP-1994; 94US-00300082.
 XX PR 17-MAR-1995; 95US-00404499.
 XX PR 26-MAY-1999; 99US-00320156.
 XX
 XX (RERE-) RES DEV FOUND.
 XX
 XX Rosenblum M, Shawver LK;
 XX P-PSDB; AEB68722.
 XX
 XX WPI; 2005-561813/57.
 XX P-PSDB; AEB68722.
 XX
 XX New immunotoxins directed against c-erbB-2 related surface antigens,
 XX useful for treating neoplastic diseases, e.g. carcinoma or
 XX adenocarcinoma.
 XX
 XX Disclosure; SEQ ID NO 12; 60pp; English.
 XX
 XX The invention relates to a composition comprising a conjugate of an
 XX antibody exhibiting binding specificity for an extracellular epitope of c
 XX -erbB-2 protein and a plant derived toxin, where the toxin is
 XX pharmacologically effective against neoplastic cells and is selected from
 XX gelonin, full length recombinant gelonin, functional gelonin fragments or
 XX functional gelonin derivatives. Also described is a pharmaceutical
 XX composition comprising the composition above and a pharmaceutical
 XX vehicle. For treating neoplastic diseases, e.g. human mammary carcinomas,
 XX human ovarian carcinomas, lung carcinomas, gastric tumors, salivary gland
 XX adenocarcinomas, or colon adenocarcinomas. The present sequence encodes a
 XX scFv23-gelonin amino acid sequence, which is used in an example from the
 XX present invention.
 XX
 XX SQ Sequence 1500 BP; 432 A; 329 C; 369 G; 370 T; 0 U; 0 Other;
 XX
 XX Query Match 88.6%; Score 24.8; DB 14; Length 1500;
 XX Best Local Similarity 92.9%; Pred. No. 1.6;
 XX Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 XX
 XX QY 1 CACATGTAACAAAGACTTCATTTCGC 28
 XX |||||
 XX Db 1041 CACAATTAACAAAGACTTCATTTCGC 1068
 XX
 XX RESULT 11
 XX ABS56029
 XX ID ABS56029 standard; DNA; 1527 BP.
 XX AC ABS56029;
 XX
 XX DT 08-JAN-2003 (first entry)
 XX
 XX DE DNA encoding murine scFvMEL/G. multiflorum rGel fusion protein.
 XX
 XX KW Modified protein; reduced antigenicity; modified toxin; gelonin;
 XX designer toxin; immunotoxin; proteinaceous compound; cancer;
 XX microbial pathogenesis; acquired immunodeficiency syndrome; AIDS;
 XX autoimmune disease; hyperproliferative disorder; leukaemia; arthritis;
 XX inflammatory disease; cardiovascular disease; diabetes;
 XX pathogenic disease; cytostatic; antiarthritic; antiinflammatory;
 XX cardiant; antidiabetic; virucide; proteoacide; fungicide; antibacterial;
 XX murine; single-chain ZME-018 antibody; recombinant gelonin; rGel;
 XX scFvMEL/rGel; mutant; ds.
 XX
 XX OS Mus sp.
 XX OS Gelonium multiflorum.
 XX OS Synthetic.
 XX
 XX FH Key Location/Qualifiers
 XX FT CDS 1..1524
 XX FT /*tag= a


```
FT      /product= "scfWEL/rGel fusion protein"
XX      WO200269886-A2.
XX      12-SEP-2002.
XX      12-FEB-2002; 2002WO-US004195.
XX      12-FEB-2001; 2001US-0268402P.
XX      (RERE-) RES DEV FOUND.
XX      Rosenblum MG, Cheung L;
XX      WPI; 2002-750431/81.
XX      P-PSDB; ABG71552.
XX      Generating a modified protein with reduced antigenicity for treating
XX      cancer, AIDS, autoimmune diseases, comprises identifying a protein region
XX      antigenic in the first subject using antiserum from either the first or a
XX      second subject.
XX      Example 5; Fig 5; 176pp; English.
XX      The present invention relates to a method of generating a modified
XX      protein with reduced antigenicity while maintaining its biological
XX      activity. The method comprises identifying a region of the protein that
XX      is antigenic in a first subject using antiserum from either the first
XX      subject or a second subject of the same species as the first subject. In
XX      particular the invention discloses modified toxin compounds, for example
XX      gelonin toxin derived from Geonium multiflorum, that are truncated
XX      and/or possess reduced antigenicity. Such designer toxins have
XX      therapeutic, diagnostic, and preventative benefits, particularly as
XX      immunotoxins. The method of the invention is useful for generating
XX      proteinaceous compounds with less antigenicity. The immunotoxin and
XX      gelonin toxin are useful for treating cancer, e.g. prostate, lung, brain,
XX      skin, liver, breast, lymphoid, stomach, testicular, ovarian, pancreatic,
XX      bone, bone marrow, head and neck, cervical, oesophagus, eye, gall
XX      bladder, kidney, adrenal glands, heart, colon, or blood cancer. The
XX      compositions of the invention are also useful for treating microbial
XX      diseases, acquired immunodeficiency syndrome (AIDS), autoimmune
XX      diseases, hyperproliferative disorders including cancer, leukaemia,
XX      arthritis, inflammatory diseases, cardiovascular diseases, pathogenic
XX      diseases, and diabetes. The method provides less antigenic proteins,
XX      peptides and polypeptides, which are more effective than prior art. The
XX      present sequence encodes murine single-chain ZME-018 antibody/G.
XX      multiflorum recombinant gelonin (rGel) (scfWEL/rGel) fusion protein
XX      SQ      Sequence 1527 BP; 458 A; 320 C; 367 G; 382 T; 0 U; 0 Other;
XX      Query Match      88.6%; Score 24.8; DB 6; Length 1527;
XX      Best Local Similarity 92.9%; Pred. No. 1.7;
XX      Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX      Qy      1 CACATGTAACACAGACTTCATTTGGC 28
XX      Db      1071 CACATTAACACAGACTTCATTTGGC 1098
XX      RESULT 12
XX      ABD32682
XX      ID      ABD32682 standard; DNA; 38142 BP.
XX      AC      ABD32682;
XX      XX      18-NOV-2004 (first entry)
XX      DE      Mouse cancer-associated genomic DNA MD13-117.
XX      KW      Mouse; ds; cancer-associated protein; gene; cytostatic; cancer;
XX      leukaemia; lymphoma; CAP.
XX      OS      Mus musculus.
```

```
XX      WO2004074320-A2.
XX      02-SEP-2004.
XX      17-FEB-2004; 2004WO-US004730.
XX      14-FEB-2003; 2003US-00367094.
XX      14-MAR-2003; 2003US-00388838.
XX      15-APR-2003; 2003US-00417375.
XX      13-JUN-2003; 2003US-00461862.
XX      15-SEP-2003; 2003US-00663431.
XX      15-DEC-2003; 2003US-00737318.
XX      (SAGR-) SAGRES DISCOVERY INC.
XX      Morris DW, Morris DW, Malandro MS;
XX      WPI; 2004-652914/63.
XX      New isolated cancer-associated polynucleotides and polypeptides useful
XX      for diagnosing, preventing or treating cancers, especially lymphoma and
XX      leukemia, or in screening for agents that modulate cancer.
XX      disclosure; seqid 236; 310pp; English.
XX      The invention relates to an isolated nucleic acid comprising at least 10
XX      contiguous nucleotides of any of the 233 polynucleotide sequences given
XX      in the specification, or its complement. The nucleic acids encode cancer-
XX      associated proteins. Also included are an expression vector comprising
XX      the isolated nucleic acid cited above, a host cell comprising the above
XX      recombinant nucleic acid or expression vector, a microarray for detecting
XX      a cancer-associated (CA) nucleic acid comprising at least one probe
XX      comprising at least 10 contiguous nucleotides of any of the above-
XX      mentioned nucleotide sequences, an isolated polypeptide (encoded within
XX      an open reading frame of a CA sequence selected from any of the 95
XX      polynucleotide sequences as mentioned in the specification, or its
XX      complement), an isolated antibody, (or its antigen binding fragment) that
XX      binds to the above polypeptide, a hybridoma that produces the above
XX      monoclonal antibody, a pharmaceutical composition comprising the above
XX      antibody and a pharmaceutical excipient, a kit for detecting cancer
XX      cells (comprising the antibody cited above, methods for diagnosing cancer
XX      or for detecting the presence or absence of cancer cells in an
XX      individual, a method for inhibiting growth of cancer cells in an
XX      individual, a method for delivering a therapeutic agent to cancer cells
XX      in an individual, an electronic library comprising the above
XX      polynucleotide or polypeptide (or their fragments), methods of screening
XX      for anticancer activity or for a bioactive agent capable of modulating
XX      the activity of a CA protein (CAP), methods for detecting cancer
XX      associated with expression of a polypeptide in a test cell sample, a
XX      method for treating cancers and a method for inhibiting the expression of
XX      CA gene in a cell. The composition and methods are useful for detecting,
XX      diagnosing, preventing and treating cancers, especially lymphoma and
XX      leukaemia. These may also be used in screening for agents that modulate
XX      cancer. The present sequence is a mouse CAP genomic sequence. Note: The
XX      sequence data for this patent did not form part of the printed
XX      specification, but was obtained in electronic format directly from WIPO
XX      at ftp.wipo.int/pub/published_pct_sequences
XX      SQ      Sequence 38142 BP; 10396 A; 8310 C; 8130 G; 10863 T; 0 U; 443 Other;
XX      Query Match      73.6%; Score 20.6; DB 13; Length 38142;
XX      Best Local Similarity 85.2%; Pred. No. 1.3e+02;
XX      Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX      Qy      1 CACATGTAACACAGACTTCATTTGG 27
XX      Db      16568 CAGATCGAACAACAGACTTCAGTGTGG 16594
XX      RESULT 13
XX      ACF73271
XX      ID      ACF73271 standard; DNA; 2103 BP.
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XX ACF73271;
AC
XX 20-NOV-2003 (first entry)
DT
XX Staphylococcus aureus DNA #951.
DE
XX Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;
KW enzymatic assay; antibiotic target; gene; ds.
KW
XX Staphylococcus aureus.
OS
XX WO200294868-A2.
PN
XX 28-NOV-2002.
PD
XX 27-MAR-2002; 2002WO-IB002637.
PF
XX 27-MAR-2001; 2001GB-00007661.
PR
XX (CHIR-) CHIRON SPA.
PA
XX Masignani V, Mora M, Scarselli M;
PI
XX WPI; 2003-120786/11.
DR
XX P-PSDB; ABW71711.
DR
XX New Staphylococcus aureus protein, useful as a vaccine for treating or
PT preventing Staphylococcal infection, specifically an infection caused by
PT S. aureus, e.g. sepsis.
XX
XX Claim 6; SEQ ID NO 1901; 49pp; English.
PS
XX The invention relates to novel genes and encoded proteins from
CC Staphylococcus aureus. A composition comprising the S. aureus protein, a
CC nucleic acid encoding the protein, or an antibody to the protein, is
CC useful as a pharmaceutical, particularly as a vaccine for treating or
CC preventing infection due to Staphylococcus bacteria, specifically an
CC infection caused by S. aureus. The composition is particularly useful for
CC treating or preventing sepsis in a patient. The composition can also be
CC used for diagnostics. The protein is also used in an assay for enzymatic
CC studies and as a target for antibiotics. This sequence represents one of
CC the novel S. aureus genes of the invention
XX
XX Sequence 2103 BP; 786 A; 330 C; 271 G; 716 T; 0 U; 0 Other;
SQ
Query Match 72.1%; Score 20.2; DB 8; Length 2103;
Best Local Similarity 88.0%; Pred. No. 1.5e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CACATGTTAAACAAGACTTCATTTT 25
DB 1838 CAGACGTAAACAAGACTTCATTTT 1862
RESULT 14
AAV74640
ID AAV74640 standard; DNA; 2187 BP.
XX
XX AAV74640;
AC
XX 16-MAR-1999 (first entry)
DT
XX Staphylococcus aureus contig SEQ ID #329.
DE
XX Computer readable medium; vaccine; S. aureus infection; immunodetection;
KW cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
KW skin infection; surgical wound infection; scalded skin syndrome;
KW toxic shock syndrome; ds.
XX
XX Staphylococcus aureus.
OS
XX
XX Key Location/Qualifiers
FH

```

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FT misc_feature 1321..1380
FT /*tag= a
FT /note= "these bases represent a line of missing text in
FT the sequence listing in the specification. They are
FT included to maintain the nucleotide numbering given in
FT the specification for this DNA sequence"
XX
XX EP786519-A2.
PN
XX 30-JUL-1997.
PD
XX 07-JAN-1997; 97EP-00100117.
PF
XX 05-JAN-1996; 96US-0009861P.
PR
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX Kunsch CA, Choi GH, Barash SC, Dillon PJ, Fannon MR, Rosen CA;
PI
XX WPI; 1997-374922/35.
XX
XX Polynucleotide(s) and proteins derived from Staphylococcus aureus -
PT stored on computer readable medium and used in the production of anti-
PT S. aureus vaccines.
XX
XX Claim 1; Page 1197-1198; 3271pp; English.
PS
XX This sequence represents one of 5191 Staphylococcus aureus DNA sequences
CC of the invention. The DNA sequences are recorded on a computer readable
CC medium, preferably selected from a floppy or hard disk, random access
CC memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using
CC the S. aureus DNA sequences allows putative functions to be assigned so
CC that protein-encoding or regulatory regions of commercial, therapeutic or
CC industrial importance can be obtained. Specifically, sequences which are
CC likely to encode antigens have been identified and these polypeptides can
CC be used in a vaccine composition against S. aureus infection. The
CC polypeptides can also be used in a kit for the immunodetection of
CC S. aureus in a sample. S. aureus is implicated in numerous human diseases,
CC including cellulitis, eyelid infections, food poisoning, osteomyelitis,
CC skin and surgical wound infections, scalded skin syndrome, toxic shock
CC syndrome, etc. Organisms transformed with the DNA sequences can be used
CC for recombinant production of the polypeptides. The new DNA sequences
CC (and their fragments) are useful as primers or probes for isolating
CC homologues of any of the S. aureus DNA sequences contained on the computer
CC readable medium
XX
XX Sequence 2187 BP; 780 A; 328 C; 334 G; 683 T; 0 U; 62 Other;
SQ
Query Match 72.1%; Score 20.2; DB 2; Length 2187;
Best Local Similarity 88.0%; Pred. No. 1.5e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CACATGTTAAACAAGACTTCATTTT 25
DB 451 CAGACGTAAACAAGACTTCATTTT 475
RESULT 15
AAT86756
ID AAT86756 standard; DNA; 11298 BP.
XX
XX AAT86756;
AC
XX 12-DEC-1997 (first entry)
DT
XX Human high affinity IgE receptor beta chain E237G variant gene.
DE
XX human; immunoglobulin E; high affinity receptor; beta subunit; IgE;
KW Fc epsilon RI beta; exon 7; variant; E237G; atopy; atopic asthma;
KW detection; diagnosis; polymorphism; subgroup; clinical management; ss.
XX
XX Homo sapiens.
OS
XX
XX

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Location/Qualifiers

FH Key 354. .511
FT exon /*tag= a
FT /number= 1
FT intron 512. .1380
FT /*tag= b
FT /number= 1
FT exon 1381. .1510
FT /*tag= c
FT intron /number= 2
FT 1511. .2025
FT /*tag= d
FT /number= 2
FT exon 2026. .2160
FT /*tag= e
FT intron /number= 3
FT 2161. .4474
FT /*tag= f
FT /number= 3
FT exon 4475. .4531
FT /*tag= g
FT intron /number= 4
FT 4532. .5078
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FT exon 5079. .5237
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FT intron /number= 5
FT 5238. .5639
FT /*tag= j
FT /number= 5
FT exon 5640. .5738
FT /*tag= k
FT intron /number= 6
FT 5739. .7223
FT /*tag= l
FT /number= 6
FT exon 7224. .10214
FT /*tag= m
FT /number= 7
FT variation 7297
FT /*tag= n
FT /note= "nucleotide change from wild type adenine to
FT guanine"
PN WO9708338-A1.
XX PD 06-MAR-1997.
XX PF 29-AUG-1996; 96WO-GB002095.
XX PR 29-AUG-1995; 95GB-00017585.
XX PA (ISIS-) ISIS INNOVATIONS LTD.
XX PI Cookson WOC, Hill MR;
XX WPI; 1997-179293/16.
XX P-PSDB; AAW29149.
XX Diagnosing atopy, or predisposition to it - by detection of
PT immunoglobulin E high affinity receptor beta subunit exon 7 variant
PT Glu237Gly.
XX PS Disclosure; Page; 25pp; English.
XX This DNA encodes human immunoglobulin E (IgE) high affinity receptor beta
CC subunit (Fc epsilon RI beta) exon 7 variant E237G. This variant is
CC associated with atopy and atopic asthma. The variation is in exon 7 and
CC is a nucleotide change from adenine to guanine at nucleotide 7297
CC (nucleotide 6843 in the Fc epsilon RI beta gene sequence of Kuster, et
CC al. 1992). Detection of the protein is useful for diagnosis of atopy. In
CC particular the E273G polymorphism may also define a subgroup of asthma

CC suffers with a particular clinical course, in which case recognition of
CC the variant/polymorphism would be of value in defining asthma prognosis
CC and management. NB. This sequence was created using the sequence given in
CC Genbank M89796
XX
SQ Sequence 11298 BP; 3469 A; 2113 C; 2284 G; 3415 T; 0 U; 17 Other;
Query Match 71.4%; Score 20; DB 2; Length 11298;
Best Local Similarity 82.1%; Pred. No. 2.1e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 CACATGTAAACAAGACTTCATTGTC 28
||||| ||||||| ||||||| |||||
Db 4423 CACATTGAAACAAGACTTCATTGTC 4450
Search completed: February 13, 2006, 00:02:17
Job time : 273 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 14, 2006, 04:02:19 ; Search time 1924 Seconds
(without alignments)
680.893 Million cell updates/sec

Title: US-10-717-243-59
Perfect score: 28
Sequence: 1 CACATGTAACACAGACTTCATTGTCG 28

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues
Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_hic:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22.2	79.3	540	10 BX992195	Forward s
2	21.6	77.1	835	11 CNS03C2M	AL237271 Tetraodon
3	21.6	77.1	1013	9 CC279684	CH261-76J
4	21.6	77.1	1128	9 CC214234	CH261-74J
5	21.2	75.7	834	7 CO646793	CO646793 ILLUMIGEN
6	21.2	75.7	942	4 AY066661	Schmidtea
7	20.8	74.3	464	2 BE581909	BS581909 kg56c05.y
8	20.8	74.3	642	10 BX199941	BX199941 Danilo rer
9	20.8	74.3	652	9 CE147952	CE147952 tigr-ges-
10	20.6	73.6	546	9 BH341834	BH341834 CH230-64B
11	20.6	73.6	576	7 CN951902	CN951902 Ha mx0.53
12	20.6	73.6	598	5 BX859292	BX859292 BX859292
13	20.6	73.6	659	11 CR033848	CR033848 Forward s
14	20.6	73.6	725	7 CN949957	CN949957 Ha mx0.27
15	20.6	73.6	759	9 BZ462328	BZ462328 BOOAA76TR
16	20.6	73.6	768	2 BG921708	BG921708 602825533
17	20.6	73.6	789	9 AQ049899	AQ049899 nbx50003a
18	20.6	73.6	802	10 CZ307473	CZ307473 ZMMPF0003
19	20.6	73.6	825	10 CW715575	CW715575 A1AA-aab9
20	20.2	72.1	443	1 AV887297	AV887297 AV887297
21	20.2	72.1	456	1 AV998061	AV998061 AV998061
22	20.2	72.1	495	8 DN897715	DN897715 nap24h08.

23	20.2	72.1	529	2 BG949978	BG949978 PM2-BN013
24	20.2	72.1	556	6 CD665396	CD665396 EtESTeg43
25	20.2	72.1	682	10 CW104570	CW104570 104_473_1
26	20.2	72.1	690	10 CW173871	CW173871 104_585_1
27	20.2	72.1	693	10 CW094316	CW094316 104_457_1
28	20.2	72.1	857	10 DU070222	DU070222 137839 To
29	20.2	72.1	875	10 CNS02890	AL211653 Tetraodon
30	20.2	72.1	880	10 CL677144	BZ229732 CH230-527
31	20.2	72.1	882	9 BZ229732	CZ317278 ZMMPF0017
32	20.2	72.1	919	10 CZ317278	BG627700 CC-esf1cL
33	20	71.4	361	2 BG627700	CO081295 GR_Ea45E
34	20	71.4	396	7 CO081295	BIS12246 BBI60008B
35	20	71.4	407	3 B512246	BIS11101 BBI60004B
36	20	71.4	466	3 B511101	AI432231 th43c06.x
37	20	71.4	494	1 AI432231	BF567678 UI-R-B00-
38	20	71.4	555	2 BF567678	CO096633 GR_Ea24K
39	20	71.4	555	7 CO096633	CO094320 GR_Ea16F
40	20	71.4	651	7 CO094320	BG127096 EST472742
41	20	71.4	663	2 BG127096	CO496608 G.h.fbr-s
42	20	71.4	683	7 CO496608	CO091583 GR_Ea12C
43	20	71.4	688	7 CO091583	CW381543 fB5001f0
44	20	71.4	751	10 CW381543	DU027161 7874 Toma
45	20	71.4	788	10 DU027161	

ALIGNMENTS

RESULT 1
BX992195 540 bp DNA linear GSS 05-JUL-2004
LOCUS Forward strand read from insert in 3'HPRT insertion targeting and
DEFINITION chromosome engineering clone MHP232j24, genomic survey sequence.
ACCESSION BX992195
VERSION BX992195.1 GI:49723653
KEYWORDS GSS; genome survey sequence; MICR.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 540)
ADAMS.D.J., BIGGS.P.J., COX.A.V., DAVIES.R.M., VAN DER WEYDEN.L.,
JONKERS.J., SMITH.J., PLUMB.R.W., TAYLOR.R.G., NISHIJIMA.I., YU.Y.,
ROGERS.J. and BRADLEY.A.
TITLE Direct Submission
JOURNAL Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. http://www.sanger.ac.uk/MICR
FEATURES
Location/Qualifiers
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/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="MHP232j24"
/clone_lib="MHP"
ORIGIN
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Best Local Similarity 88.9%; Pred. No. 2.4e+02;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CACATGTAACACAGACTTCATTGTCG 27
Db 275 CACATGTAGCACAGACTGCATTGTCG 301
CNS03C2M 835 bp DNA linear GSS 01-SEP-2000
LOCUS Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
DEFINITION 013B17 of library G from tetraodon nigroviridis, genomic survey
sequence.
ACCESSION AL237271

VERSION	AL237271.1	GI:7896406
KEYWORDS	GSS; genome survey sequence.	
SOURCE	Tetraodon nigroviridis	
ORGANISM	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorphia; Tetraodontiformes; Tetraontoidea; Tetraodontidae; Tetraodon.	
REFERENCE	1	Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Surin,W. and Weissenbach,J.
AUTHORS		Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence
TITLE		Nat. Genet. 25 (2), 235-238 (2000)
JOURNAL		10835645
PUBLISHED		
REFERENCE	2	Roest Crolius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C., Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F., Surin,W., Bernot,A. and Weissenbach,J.
AUTHORS		Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
TITLE		Genome Res. 10 (7), 939-949 (2000)
JOURNAL		
PUBLISHED		10899143
REFERENCE	3	(bases 1 to 835)
AUTHORS		Genoscope.
TITLE		Direct Submission
JOURNAL		Submitted (12-APR-2000) Genoscope - Centre National de Sequences : BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr
COMMENT		- Web : www.genoscope.cns.fr) This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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		/organism="Tetraodon nigroviridis"
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		/clone_lib="G"
		/note="Genoscope sequence ID : C0BG013CA09SP1 end : PUC-ori"
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Best Local Similarity	85.77;	Pred. No. 4.4e+02;
Matches	24;	Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY	1	CACATGTAAACACAGACTTCATTGTGGC 28
DB	270	CAATATGAAACACAGACTTTATTGTGC 297
RESULT 3		
CC279684/c		
LOCUS	CH261-76220_RM1.1	CH261 Gallus gallus genomic clone CH261-76J20, 1013 bp DNA linear GSS 13-MAY-2003
DEFINITION		genomic survey sequence.
ACCESSION	CC279684	
VERSION	CC279684.1	GI:30642252
KEYWORDS		GSS.
SOURCE		Gallus gallus (chicken)
ORGANISM		Gallus gallus
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
REFERENCE		1 (bases 1 to 1013)
AUTHORS		Kremitzki,C., Higginbotham,J., Wylie,K., Carter,J., McPherson,J., Warren,W., Graves,T., Mardis,E. and Wilson,R.
TITLE		Gallus gallus BAC End Reads
COMMENT		Unpublished (2003) Contact: Richard K. Wilson


```

Query Match      77.1%; Score 21.6; DB 9; Length 1128;
Best Local Similarity 85.7%; Pred. No. 4.6e+02;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CACATGTAATAAAGACTTCATTTCG 28
Db 312 CACTGTGAAGACATGACTTCATTTCG 285

RESULT 5
CO646793
LOCUS
DEFINITION
ILLUMIGEN MCQ_39642 Katze_MPB2 Macaca mulatta cDNA clone
IBIW:22782 5' similar to Bases 5 to 734 highly similar to human
WDR36 [Hs.175596], mRNA sequence.
ACCESSION
CO646793
VERSION
KEYWORDS
SOURCE
ORGANISM
Macaca mulatta (rhesus monkey)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Cercopithecoidea; Cercopithecinae; Macaca.
REFERENCE
1 (bases 1 to 834)
Magness,C.L., Fellin,P.C., Thomas,M.J., Korth,M.J., Agy,M.B.,
Prohl,S.C., Fitzgibbon,M., Scherer,C.A., Miner,D.G., Katze,M.G. and
Iadonato,S.P.
Iadonato,S.P.
TITLE
Analysis of the Macaca mulatta transcriptome and the sequence
divergence between Macaca and human
JOURNAL
Genome Biol. 6 (7), R60 (2005)
PUBMED
15998449
COMMENT
Contact: C. Magness
Email: cmagness@illumigen.com
Illumigen Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
Tel: 2063780400
Fax: 2063780408
Email: cmagness@illumigen.com
Sequenced on 2004.05.27. 681 Q20 bases. Library Preparation: Prof.
Michael Katze Lab at University of Washington DNA Sequencing:
Illumigen Biosciences Inc. For further information, see
http://www.macaque.org

PCR Primers
FORWARD: CCTCACTAAAGGGACAA
BACKWARD: CACTATAGGGCGAATTCGGTA
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POLYA=No.

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/clone_lib="Katze_MPB2"
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Created from CloneMiner cDNA Library Construction kit
(catalog #18249-029)"

ORIGIN
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Best Local Similarity 88.5%; Pred. No. 6.5e+02;
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CACATGTAATAAAGACTTCATTTCG 26
Db 312 CACTGTGAAGACATGACTTCATTTCG 285

RESULT 6
CO646661
LOCUS
DEFINITION
Schmidtea mediterranea clone H.25.6h unknown mRNA sequence.
ACCESSION
AY066661
VERSION
AY066661.1 GI:24796201
KEYWORDS
HTC.
SOURCE
Schmidtea mediterranea
ORGANISM
Schmidtea mediterranea
Eukaryota; Metazoa; Platyhelminthes; Turbellaria; Seriate;
Tricladida; Paludicola; Dugesidae; Schmidtea.
REFERENCE
1 (bases 1 to 942)
Alvarado,A.S., Newmark,P.A., Robb,S.M.C. and Juste,R.B.
The Schmidtea mediterranea database as a molecular resource for
studying plathyelminthes, stem cells and regeneration
Development 129 (24), 5659-5665 (2002)
JOURNAL
12421706
PUBMED
12421706
AUTHORS
Alvarado,A.S., Newmark,P.A., Juste,R.B. and Robb,S.M.C.
Direct Submission
TITLE
Submitted (07-DEC-2001) Neurobiology & Anatomy, University of Utah
School of Medicine, 50 North Medical Drive, Salt Lake City, UT
84132, USA
COMMENT
Clone names suffixed with 'T3' were sequenced from their 5' ends.
All other clones were obtained by sequencing from their 3' ends.
More details and other relevant information can be found at
http://planaria.neuro.utah.edu.
FEATURES
source
Location/Qualifiers
1..942
/organism="Schmidtea mediterranea"
/mol_type="mRNA"
/strain="CIW4"
/db_xref="taxon:79327"
/clone="H.25.6h"
1..942
/notes="similar to (BC004070) Unknown (protein for
MGC:8213) Mus musculus"

ORIGIN
Query Match      75.7%; Score 21.2; DB 4; Length 942;
Best Local Similarity 88.5%; Pred. No. 6.6e+02;
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ACATGTAATAAAGACTTCATTTCG 27
Db 399 AAATGAAACACAGACTTCATTTCG 374

RESULT 7
BE581909
LOCUS
DEFINITION
kq56c05.y1 TBN95TM-SSR Strongyloides stercoralis cDNA 5' similar to
WP.Y113G7A.11 CB23282, mRNA sequence.
ACCESSION
BE581909
VERSION
BE581909.1 GI:9832851
KEYWORDS
EST.
SOURCE
Strongyloides stercoralis
ORGANISM
Strongyloides stercoralis
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Panagrolaimidae; Strongyloidea; Strongyloides.
REFERENCE
1 (bases 1 to 464)
McCarte,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J.,
Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B.,
Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C.,
Tsagarishvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C.,
Underwood,K., Steptoe,M., Allen,M., Person,B., Swaller,T.,
Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
McCann,R., Waterston,R. and Wilson,R.
The Washington Univ. Nematode EST Project, 1999
Unpublished (1999)
JOURNAL

```


COMMENT

Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
The library was constructed by Dr. Thomas Nutman and colleagues of NIAID, NIH (tnutman@nih.gov). DNA sequencing by: Washington University Genome Sequencing Center St. Louis.
High quality sequence stop: 262.

FEATURES

source

1..464
/organism="Strongyloides stercoralis"
/mol_type="mRNA"
/strain="Rhabditiform larvae obtained from gerbils"
/db_xref="taxon:6248"
/lab_host="XL-1 Blue MRP" (Stratagene)"
/clone_lib="TBN95TM-SSR"
/note="Vector: Lambda Uni-ZAP XR (Stratagene); Site 1: EcoRI; Site 2: XhoI; mRNA was purified from 2 x 10E3 rhabditiform larvae which had been isolated from gerbils experimentally infected with larvae originally isolated from experimentally infected dogs. cDNA was constructed and, using adaptors, was cloned unidirectionally into the vector from the EcoRI site to the XhoI site. The library has an unamplified titer of 1 x 10E5 pfu/ml and an amplified, undiluted titer of 9 x 10E11 pfu/ml. The average insert size of the unamplified library is 675 bp (range, 100-1700)."

ORIGIN

Query Match 74.3%; Score 20.8; DB 2; Length 464;
Best Local Similarity 91.7%; Pred. No. 8.7e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 ATGTAAACACAGACTTCATTGG 27

DB 109 ATGGAACACAGACTTCCTTTGG 132

RESULT 8

BX199941/c

LOCUS Danio rerio genomic clone DKRY-208J5, linear GSS 13-MAR-2003
DEFINITION Danio rerio genomic clone DKRY-208J5, genomic survey sequence.
ACCESSION BX199941
VERSION BX199941.1 GI:28031827

KEYWORDS

GSS

SOURCE Danio rerio (zebrafish)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.

REFERENCE

1 (bases 1 to 642)

AUTHORS Humphray, S.J., Huckle, E. and Durham, J.L.

TITLE Direct Submission

JOURNAL Submitted (13-MAR-2003) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk Unpublished

COMMENT

This sequence was generated from the T7 end of BAC 208J5. 208J5 is part of the Daniokey BAC Library created by R. Plasterk and N.V. Keygene. Further details:
http://www.sanger.ac.uk/Projects/D_rerio/.

FEATURES

source

1..642
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKRY-208J5"
/tissue_type="Testis"
/note="vector pIndigoBAC-536"

ORIGIN

Query Match 74.3%; Score 20.8; DB 10; Length 642;
Best Local Similarity 91.7%; Pred. No. 9.1e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CACATGTAAACACAGACTTCATT 24

DB 308 CACATGTAAACACAGACTTCATT 285

RESULT 9

CE147952/c

LOCUS

DEFINITION

CE147952

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Canis familiaris (dog)

Canis familiaris

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;

Canis.

REFERENCE

1 (bases 1 to 652)

AUTHORS Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,

Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and

Venter, J.C.

TITLE The dog genome: survey sequencing and comparative analysis

JOURNAL Science 301 (5641), 1898-1903 (2003)

PUBMED 14512627

COMMENT Contact: Kirkness EF

The Institute for Genomic Research

Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,

Rockville, MD 20850, USA

Tel: 301-838-0200

Fax: 301-838-0208

Email: ekirknes@tigr.org

Class: shotgun.

Location/Qualifiers

1..652

/organism="Canis familiaris"

/mol_type="genomic DNA"

/strain="Standard Poodle"

/db_xref="taxon:9615"

/clone_lib="Dog Library"

/note="Site 1: BstXI; Libraries were prepared from

peripheral blood"

ORIGIN

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

0;

QY 4 ATGTAAACACAGACTTCATTGG 27

DB 309 ATGGAACACAGACTTCATTGG 286

RESULT 10

BH341834

LOCUS

DEFINITION

BH341834

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Rattus norvegicus (Norway rat)

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE

1 (bases 1 to 546)

AUTHORS Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K.,

Shvartabeyn, A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D.,


```

Seq primer: SP6
High quality sequence stop: 477.
Location/Qualifiers
1. .576
/organism="Homoarum americanus"
/mol_type="mRNA"
/db_xref="taxon:6706"
/clone="Ha_mx0_53e01"
/tissue_type="Gill, epipodite, branchiostegite, heart,
ovary, testis, antennal gland, abdominal muscle,
hepatopancreas, brain"
/dev_stage="Adult intermolt"
/clone_lib="Lobster Multiple Tissues, Normalized"
/note="Vector: pCMV Sport 6.1; Total RNA samples were
prepared individually from each tissue, checked for
quality, then pooled for construction and normalization
of cDNA library by Invitrogen. Plasmids were isolated
and inserts end-sequenced by the Marine DNA Sequencing and
Analysis Facility at Mount Desert Island Biological
Laboratory. Traces were processed for submission to
dBSST by tracedbest software (Parkinson, Anthony and
Blaxter, unpublished software)."
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ORIGIN

Query Match	73.6%;	Score 20.6;	DB 7;	Length 576;
Best Local Similarity	85.2%;	Pred. No. 1.1e+03;		
Matches 23;	Conservative 0;	Mismatches 4;	Indels 0;	Gaps 0;

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QY      1  CACATGTAACACAGACTTCATTGCG 27
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DB      63  CACATACCAAGAAGACTTCATTGCG 37
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RESULT	12
EX859292	
LOCUS	
DEFINITION	EX859292 ACENAE Rainbow trout normalized testis library (ccbl)
	Oncorhynchus mykiss cdna clone tcbi001ld.p.11 Sprim, mRNA sequence.
ACCESSION	EX859292
VERSION	EX859292.2 GI:42756060
KEYWORDS	EST.
SOURCE	Oncorhynchus mykiss (rainbow trout)

ORGANISM
 Oncorhynchus mykiss
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
REFERENCE
 1 (bases 1 to 598)
 Govoroun M., Guiguen Y. and Le Gac F.
AUTHORS
 Construction and primary characterization of normalized cDNA
 libraries in rainbow trout, *Oncorhynchus mykiss*
TITLE
 Unpublished (2003)
JOURNAL
 On Dec 16, 2003 this sequence version replaced gi:39956980.
COMMENT
 Contact: Guiguen Y
 INRA - SCRIBE
 Campus de beaulieu, RENNES cedex, 35042, France
 Tel: 02.23.48.50.09
 Fax: 02.23.48.50.20
 Email: Yann.Guiguen@beaulieu.rennes.inra.fr
 Sequence cleaned of vector, adaptor and repetitions. Contact us
 at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
 sequence.
 Plate: 0011 row: p column: 11
 Seq primer: M13R.
FEATURES
 Location/Qualifiers
 1..598
 /organism="Oncorhynchus mykiss"
 /mol_type="mRNA"
 /db_xref="taxon:8022"
 /clone="tcbi0011d.p.11"
 /tissue_type="testis"
 /lab_host="DH10B"
 /clone_lib="AGENAE Rainbow trout normalized testis library
 (tcbi)"

/note="Vector: pT7T3D-pac; Clone distribution : AGENAE Resource centre, Francois PIUMI, Francois.Plumiojony.inra.fr, INRA, CEA Radiobiologie et Etude du genome (JREG), Domaine de Vilvert, 78352, Jouy-en-Josas cedex, FRANCE, +33 (0) 1.34.65.28.02, +33 (0) 1.34.65.22.73"

ORIGIN

Query Match 73.6%; Score 20.6; DB 5; Length 598;
Best Local Similarity 85.2%; Pred. No. 1.1e+03;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ACATGTAAACAGACTTCATTTCGC 28

Db 550 ACATGCAAGACAGACATCATTTTGC 576

RESULT 13

CR033848

LOCUS 659 bp DNA linear GSS 05-JUL-2004
DEFINITION Forward strand read from insert in 3'HPRT insertion targeting and chromosome engineering clone MHP232123, genomic survey sequence.

ACCESSION CR033848

VERSION 1

KEYWORDS GSS; genome survey sequence; MICER.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.

AUTHORS 1 (bases 1 to 659)

ADAMS,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L., Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y., Rogers,J. and Bradley,A.

TITLE Direct Submission

JOURNAL Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,

CB10 1SA, UK. http://www.sanger.ac.uk/MICER

FEATURES

source

1..659

/organism="Mus musculus"

/mol_type="genomic DNA"

/db_xref="taxon:10090"

/clone="MHP232123"

/clone_lib="MHP"

ORIGIN

Query Match 73.6%; Score 20.6; DB 11; Length 659;
Best Local Similarity 85.2%; Pred. No. 1.1e+03;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CACATGTAAACAGACTTCATTTCG 27

Db 275 CACATGTAGCAGGACTGCTATTTCG 301

RESULT 14

CN949957/c

LOCUS

DEFINITION Ha_mx0 27a03 SP6 Lobster Multiple Tissues, Normalized Homarus americanus cDNA clone Ha_mx0 27a03 5' similar to ref|XP_309809.1| ENSANGP0000018221 - Anopheles gambiae. Score = 251 bits (641), Expect = 1e-65, mRNA sequence.

ACCESSION CN949957

VERSION 1

KEYWORDS EST.

SOURCE Homarus americanus (American lobster)

ORGANISM Homarus americanus

REFERENCE Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea; Nephropoidea; Nephropidae; Homarus.

AUTHORS 1 (bases 1 to 725)

Towle,D.W. and Smith,C.M.

TITLE Expressed sequence tags in a normalized cDNA library prepared from

multiple tissues of adult intermolt American lobster, Homarus americanus

JOURNAL

COMMENT

Unpublished (2004)
Contact: David W. Towle
Marine DNA Sequencing and Analysis Center
Mount Desert Island Biological Laboratory
Old Bar Harbor Road, Salsbury Cove, ME 04672 USA

Tel: 207-288-9880 x474

Fax: 207-288-2130

Email: dtowle@mdibl.org

Plate: 27 row: a column: 03

Seq primer: SP6

High quality sequence stop: 501.

FEATURES

source

1..725

/organism="Homarus americanus"

/mol_type="mRNA"

/db_xref="taxon:6706"

/clone="Ha_mx0 27a03"

/tissue_type="Gill, epipodite, branchiostegite, heart,

ovary, testis, antennal gland, abdominal muscle,

hepatopancreas, brain"

/dev_stages="Adult intermolt"

/note="Vector: pCMV Sport 6.1; Total RNA samples were

prepared individually from each tissue, checked for

quality, then pooled for construction and normalization

of cDNA library by Invitrogen. Plasmids were isolated

and inserts end-sequenced by the Marine DNA Sequencing and

Analysis Facility at Mount Desert Island Biological

Laboratory. Traces were processed for submission to

dbEST by trace2dbest software (Parkinson, Anthony and

Blaxter, unpublished software)."

ORIGIN

Query Match 73.6%; Score 20.6; DB 7; Length 725;
Best Local Similarity 85.2%; Pred. No. 1.1e+03;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CACATGTAAACAGACTTCATTTCG 27

Db 73 CACATACCACAGAGACTTCATTTCG 47

RESULT 15

BZ462328/c

LOCUS

DEFINITION BZ462328 BO 1.6.2 KB tot Brassica oleracea genomic clone BO0AA76,
Genomic survey sequence.

ACCESSION BZ462328

VERSION 1

KEYWORDS GSS.

SOURCE Brassica oleracea

ORGANISM Brassica oleracea

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

AUTHORS 1 (bases 1 to 759)

Ayele,M., Haas,B.J., Kumar,N., Wu,H., Xiao,Y., Van Aken,S.,
Utterback,T.R., Wortman,J.R., White,O.R. and Town,C.D.

Whole genome shotgun sequencing of Brassica oleracea and its

application to gene discovery and annotation in Arabidopsis

Genome Res. 15 (4), 487-495 (2005)

JOURNAL 15805490

PUBMED Other GSSs: BO0AA76TF

COMMENT Contact: Chris Town

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA.

Tel: 301-838-3523

Fax: 301-838-0208

Email: cdtown@tigr.org

DNA is from a doubled haploid provided by Tom Osborn.

Seq primer: TR


```
Class: sheared ends.
FEATURES             Location/Qualifiers
     source           1..759
                     /organism="Brassica oleracea"
                     /mol_type="genomic DNA"
                     /strain="T01000DH3"
                     /db_xref="taxon:3712"
                     /clone="BOOAA76"
                     /clone_lib="BO.1.6.2_KB_tot"
                     /note="Vector: pHO51; Site 1: BatXI; 1.6-2 kb sheared
total DNA inserted into pHO51 using BatXI linkers"

ORIGIN
Query Match      73.6%; Score 20.6; DB 9; Length 759;
Best Local Similarity 85.2%; Pred. No. 1.1e+03;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 CACATGTTAAACAAGACTTCATTTTGG 27
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Db      567 CAAATCTACATCAGACTTCATTTTGG 541

Search completed: February 14, 2006, 05:30:03
Job time : 1928 secs
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 12, 2006, 23:57:57 ; Search time 96 Seconds
(without alignments)
518.455 Million cell updates/sec

Title: US-10-717-243-59

Perfect score: 28

Sequence: 1 CACATGTAAACAGACTTCATTGTCG 28

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgm2_6/ptodata/1/ina/1 COMB.seq.*
2: /cgm2_6/ptodata/1/ina/5 COMB.seq.*
3: /cgm2_6/ptodata/1/ina/6A COMB.seq.*
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5: /cgm2_6/ptodata/1/ina/H COMB.seq.*
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8: /cgm2_6/ptodata/1/ina/RE COMB.seq.*
9: /cgm2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	100.0	28	2	US-07-988-430-61
2	28	100.0	28	2	US-08-425-336-59
3	28	100.0	28	2	US-08-488-113B-59
4	28	100.0	28	2	US-08-477-484B-59
5	28	100.0	28	2	US-08-646-360-59
6	28	100.0	28	3	US-08-839-765-59
7	28	100.0	28	3	US-09-136-389-59
8	28	100.0	28	3	US-09-610-838-59
9	28	100.0	28	3	US-09-711-485-59
10	28	100.0	28	6	PCT-US92-09487-61
11	24.8	88.6	813	2	US-07-901-707-11
12	24.8	88.6	813	2	US-07-901-707-57
13	24.8	88.6	813	2	US-07-988-430-11
14	24.8	88.6	813	2	US-07-988-430-57
15	24.8	88.6	813	2	US-08-425-336-11
16	24.8	88.6	813	2	US-08-488-113B-11
17	24.8	88.6	813	2	US-08-477-484B-11
18	24.8	88.6	813	2	US-08-646-360-11
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20	24.8	88.6	813	3	US-08-839-765-11
21	24.8	88.6	813	3	US-09-136-389-11
22	24.8	88.6	813	3	US-09-217-352-246
23	24.8	88.6	813	3	US-09-610-838-11
24	24.8	88.6	813	3	US-09-711-485-11

Sequence 11, Appl
Sequence 57, Appl
Sequence 258, App
Sequence 258, App
Sequence 252, App
Sequence 252, App
Sequence 250, App
Sequence 250, App
Sequence 329, App
Sequence 329, App
Sequence 31, Appl
Sequence 2, Appl
Sequence 31, Appl
Sequence 11750, A
Sequence 16934, A
Sequence 45, Appl
Sequence 9, Appl
Sequence 9, Appl
Sequence 16597, A
Sequence 62, Appl

25 24.8 88.6 813 6 PCT-US92-09487-11
26 24.8 88.6 813 6 PCT-US92-09487-57
27 24.8 88.6 955 2 US-08-621-803-258
28 24.8 88.6 955 3 US-09-217-352-258
29 24.8 88.6 1003 2 US-08-621-803-252
30 24.8 88.6 1003 3 US-09-217-352-252
31 24.8 88.6 1072 2 US-08-621-803-250
32 24.8 88.6 1072 3 US-09-217-352-250
33 20.2 72.1 2187 3 US-08-956-171B-329
34 20.2 72.1 2187 3 US-08-781-986A-329
35 20 71.4 11298 2 US-07-869-933-31
36 20 71.4 11298 2 US-08-201-879A-2
37 20 71.4 11298 3 US-08-103-663-31
38 20 71.4 98567 3 US-09-949-016-11750
39 20 71.4 100567 3 US-09-949-016-16934
40 19.6 70.0 2100 3 US-09-771-161A-45
41 19.6 70.0 3132 2 US-08-167-919A-9
42 19.6 70.0 3132 3 US-08-715-106-9
43 19.6 70.0 3132 3 US-03-442-649-9
44 19.6 70.0 126982 3 US-09-949-016-16597
45 19.4 69.3 36 2 US-07-988-430-62

ALIGNMENTS

RESULT 1

US-07-988-430-61
; Sequence 61, Application US/07988430
; Patent No. 5416202
; GENERAL INFORMATION:
; APPLICANT: Bernhardt, Susan L.
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Lane, Julie A.
; APPLICANT: Lei, Shau-Ping
; TITLE OF INVENTION: Materials Comprising and Methods of
; TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/988,430
; FILING DATE: 19921209
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5416202and, Greta E.
; REGISTRATION NUMBER: 35302
; REFERENCE/DOCKET NUMBER: 31133
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:

;
; LENGTH: 28 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-07-988-430-61

Query Match 100.0%; Score 28; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0044;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACATGTAACAAGACTTCATTTTGGC 28

Db 1 CACATGTAACAAGACTTCATTTTGGC 28

RESULT 2

US-08-425-336-59
; Sequence 59, Application US/08425336
; Patent No. 5621083
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425,336
; FILING DATE: 18-APR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Thomas C.
; REGISTRATION NUMBER: P-36,989
; REFERENCE/DOCKET NUMBER: 31394
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-425-336-59

Query Match 100.0%; Score 28; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0044;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACATGTAACAAGACTTCATTTTGGC 28

Db 1 CACATGTAACAAGACTTCATTTTGGC 28

RESULT 3

US-08-488-113B-59
; Sequence 59, Application US/08488113B
; Patent No. 5744580
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,113B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.CZA
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-113B-59

Query Match 100.0%; Score 28; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0044;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACATGTAACAAGACTTCATTTTGGC 28

Db 1 CACATGTAACAAGACTTCATTTTGGC 28

RESULT 4

US-08-477-484B-59
; Sequence 59, Application US/08477484B
; Patent No. 5756699
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,484B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-477-484B-59

Query Match 100.0%; Score 28; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0044;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACATGTAACAAGACTTCATTTGGC 28
DB 1 CACATGTAACAAGACTTCATTTGGC 28

RESULT 5
US-08-646-360-59
; Sequence 59, Application US/08646360
; Patent No. 5837491
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.

; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,360
; FILING DATE: 13-MAY-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-646-360-59

Query Match 100.0%; Score 28; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0044;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACATGTAACAAGACTTCATTTGGC 28
DB 1 CACATGTAACAAGACTTCATTTGGC 28

RESULT 6
US-08-839-765-59
; Sequence 59, Application US/08839765
; Patent No. 6146631
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;; STREET: 500 West Madison Street, 34th floor
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: USA
;; ZIP: 60661
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/839,765
;; FILING DATE: 15-APR-1997
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/425,336
;; FILING DATE: 18-APR-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/064,691
;; FILING DATE: 12-MAY-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/988,430
;; FILING DATE: 09-DEC-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/901,707
;; FILING DATE: 19-JUN-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/787,567
;; FILING DATE: 04-NOV-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: McNicholas, Janet M.
;; REGISTRATION NUMBER: 32,918
;; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312/707-8889
;; TELEFAX: 312/707-9155
;; TELEX: 650 388-1248
;; INFORMATION FOR SEQ ID NO: 59:
;; LENGTH: 28 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA
US-08-839-765-59

Query Match 100.0%; Score 28; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0044;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CACATGTAACAAACAGACTTCATTTTGGC 28
Db 1 CACATGTAACAAACAGACTTCATTTTGGC 28

RESULT 7
US-09-136-389-59
; Sequence 59, Application US/09136389
; Patent No. 6146850
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois

;; COUNTRY: USA
;; ZIP: 60661
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/136,389
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/646,360
;; FILING DATE: 13-MAY-1996
;; APPLICATION NUMBER: PCT/US94/05348
;; FILING DATE: 12-MAY-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/064,691
;; FILING DATE: 12-MAY-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/988,430
;; FILING DATE: 09-DEC-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/901,707
;; FILING DATE: 19-JUN-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/787,567
;; FILING DATE: 04-NOV-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: McNicholas, Janet M.
;; REGISTRATION NUMBER: 32,918
;; REFERENCE/DOCKET NUMBER: 200-70.P4
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312/707-8889
;; TELEFAX: 312/707-9155
;; TELEX: 650 388-1248
;; INFORMATION FOR SEQ ID NO: 59:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 28 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA
US-09-136-389-59

Query Match 100.0%; Score 28; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0044;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CACATGTAACAAACAGACTTCATTTTGGC 28
Db 1 CACATGTAACAAACAGACTTCATTTTGGC 28

RESULT 8
US-09-610-838-59
; Sequence 59, Application US/09610838
; Patent No. 6376217
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/610,838
FILING DATE: 06-JUL-2000
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/136,389
FILING DATE: 18-AUG-1998
APPLICATION NUMBER: 08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-610-838-59

Query Match 100.0%; Score 28; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0044;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CACATGTAACACAGACTTCATTTTGGC 28
Db 1 CACATGTAACACAGACTTCATTTTGGC 28

RESULT 9
US-09-711-485-59
Sequence 59, Application US/09711485
Patent No. 6649742
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/711,485
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/839,765
FILING DATE:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-711-485-59

Query Match 100.0%; Score 28; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0044;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CACATGTAACACAGACTTCATTTTGGC 28
Db 1 CACATGTAACACAGACTTCATTTTGGC 28

RESULT 10
PCT-US92-09487-61
Sequence 61, Application PC/TUS9209487
GENERAL INFORMATION:
APPLICANT: Bernhard, Susan L.
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Lane, Julie A.
APPLICANT: Lei, Shau-Ping
TITLE OF INVENTION: Materials Comprising and Methods of
TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
STREET: Two First National Plaza, 20 South Clark
STREET: Street
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/09487
FILING DATE: 19921104
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Noland, Greta E.
REGISTRATION NUMBER: 35302
REFERENCE/DOCKET NUMBER: 31133
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
PCT-US92-09487-61

Query Match 100.0%; Score 28; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0044;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACATGTAACAAAGACTTCATTTCGC 28
|||||
DB 1 CACATGTAACAAAGACTTCATTTCGC 28

RESULT 11
US-07-901-707-11
Sequence 11, Application US/07901707
Patent No. 5376546
GENERAL INFORMATION:
APPLICANT: Bernhardt, Susan L.
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Steve F.
APPLICANT: Lane, Julie A.
TITLE OF INVENTION: Materials Comprising and Methods of
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSER: Bicknell
STREET: Two First National Plaza, 20 South Clark
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/901,707
FILING DATE: 19920619
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 5376546and, Greta E.
REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 27129/30910
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-5750
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 813 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-07-901-707-11
Query Match 88.6%; Score 24.8; DB 2; Length 813;
Best Local Similarity 92.9%; Pred. No. 0.19;
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CACATGTAACAAAGACTTCATTTCGC 28
|||||
DB 303 CACATGTAACAAAGACTTCATTTCGC 330
RESULT 12
US-07-901-707-57
Sequence 57, Application US/07901707
Patent No. 5376546
GENERAL INFORMATION:
APPLICANT: Bernhardt, Susan L.
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Steve F.
APPLICANT: Lane, Julie A.
TITLE OF INVENTION: Materials Comprising and Methods of
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSER: Bicknell
STREET: Two First National Plaza, 20 South Clark
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/901,707
FILING DATE: 19920619
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 5376546and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27129/30910
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-5750
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 813 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-07-901-707-57


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US-07-988-430-57
; Sequence 57, Application US/07988430
; Patent No. 5416202
; GENERAL INFORMATION:
; APPLICANT: Bernhard, Susan L.
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Lane, Julie A.
; APPLICANT: Lei, Shau-Ping
; TITLE OF INVENTION: Materials Comprising and Methods of
; Preparation and Use for Ribosome-Inactivating Protein
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/988,430
; FILING DATE: 19921209
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5416202and, Greta E.
; REGISTRATION NUMBER: 35302
; REFERENCE/DOCKET NUMBER: 31133
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 813 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-07-988-430-57

Query Match      88.6%; Score 24.8; DB 2; Length 813;
Best Local Similarity 92.9%; Pred. No. 0.19;
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1  CACATCTAAACCAAGACTTCATTTGGC 28
Db      303 CACATCTAAACCAAGACTTCATTTGGC 330

RESULT 15
US-08-425-336-11
; Sequence 11, Application US/08425336
; Patent No. 5621083
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 140

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RESULT 15
US-08-425-336-11
; Sequence 11, Application US/08425336
; Patent No. 5621083
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 140

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Search completed: February 13, 2006, 00:03:57
Job time : 97 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 13, 2006, 00:55:33 ; Search time 424 Seconds
(without alignments)
546.091 Million cell updates/sec

Title: US-10-717-243-59

Perfect score: 28

Sequence: 1 CACATGTAACACAGACTTCATTGTCG 28

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA_Main:
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10: /cgm2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	28	100.0	28	9	US-10-717-243-59
3	24.8	88.6	813	3	US-09-765-527-246
4	24.8	88.6	813	6	US-10-127-890-11
5	24.8	88.6	813	9	US-10-717-243-11
6	24.8	88.6	955	3	US-09-765-527-258
7	24.8	88.6	1003	3	US-09-765-527-252
8	24.8	88.6	1072	3	US-09-765-527-250
9	24.8	88.6	1176	6	US-10-074-596-2
10	24.8	88.6	1500	9	US-10-964-195-12
11	24.8	88.6	1527	6	US-10-074-596-10
12	24.8	88.6	2407	10	US-11-084-080-25
13	21.6	77.1	600	9	US-10-972-079-84211
14	21.6	77.1	600	9	US-10-972-079-84212
15	21.6	77.1	600	9	US-10-972-079-84213
16	21.6	77.1	600	9	US-10-972-079-84214
17	20.6	73.6	38142	8	US-10-417-375-55
18	20.2	72.1	2187	2	US-08-781-986A-329
19	20.2	72.1	2187	7	US-10-329-624-329
20	20	71.4	11298	3	US-09-960-706-705
c 21	19.8	70.7	349	7	US-10-424-599-12953
c 22	19.8	70.7	742	5	US-10-027-632-141533
c 23	19.8	70.7	742	5	US-10-027-632-141534

c 24	19.8	70.7	742	6	US-10-027-632-141533	Sequence 141533,
c 25	19.8	70.7	742	6	US-10-027-632-141534	Sequence 141534,
c 26	19.8	70.7	13886	8	US-10-741-600-17592	Sequence 17592, A
27	19.6	70.0	553	4	US-09-925-065A-436767	Sequence 436767,
28	19.6	70.0	598	4	US-09-925-065A-391252	Sequence 391252,
29	19.6	70.0	2100	3	US-09-771-161A-45	Sequence 45, Appl
30	19.6	70.0	2793	9	US-10-794-514A-470	Sequence 470, Appl
31	19.6	70.0	2949	9	US-10-489-135B-12	Sequence 12, Appl
32	19.6	70.0	2952	6	US-10-345-680-3	Sequence 3, Appl
33	19.6	70.0	2953	7	US-10-384-339C-3	Sequence 3, Appl
34	19.6	70.0	3149	5	US-10-205-823-96	Sequence 96, Appl
35	19.6	70.0	3149	6	US-10-345-680-1	Sequence 1, Appl
36	19.6	70.0	3149	6	US-10-295-027-601	Sequence 601, Appl
37	19.6	70.0	3149	8	US-10-473-974-320	Sequence 220, Appl
38	19.6	70.0	3149	10	US-11-051-454-96	Sequence 96, Appl
39	19.6	70.0	5799	9	US-10-794-514A-468	Sequence 468, Appl
40	19.6	70.0	5835	8	US-10-723-860-6909	Sequence 6909, Ap
c 41	19.4	69.3	36	6	US-10-127-890-60	Sequence 60, Appl
c 42	19.4	69.3	36	9	US-10-717-243-60	Sequence 60, Appl
c 43	19.4	69.3	1223197	5	US-10-027-632-179264	Sequence 179264,
c 44	19.4	69.3	1223197	6	US-10-027-632-179264	Sequence 179264,
c 45	19.2	68.6	179	3	US-09-783-590-2798	Sequence 2798, Ap

ALIGNMENTS

RESULT 1

US-10-127-890-59
; Sequence 59, Application US/10127890
; Publication No. US20030166196A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Carroll, Stephen F.
; Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/127,890
; FILING DATE: 23-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889


```
;
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 59:
US-10-127-890-59

Query Match      100.0%; Score 28; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.073;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CACATGTAATAACAAGACTTCATTTTGGC 28
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DB      1 CACATGTAATAACAAGACTTCATTTTGGC 28

RESULT 2
US-10-717-243-59
; Sequence 59, Application US/10717243
; Publication No. US20050054835A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
;           Carroll, Stephen F.
;           Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;                     Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/717,243
; FILING DATE: 18-Nov-2003
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/839,765
; FILING DATE: 15-APR-1997
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
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;
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 59:
US-10-717-243-59

Query Match      100.0%; Score 28; DB 9; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.073;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CACATGTAATAACAAGACTTCATTTTGGC 28
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DB      1 CACATGTAATAACAAGACTTCATTTTGGC 28

RESULT 3
US-09-765-527-246
; Sequence 246, Application US/09765527
; Patent No. US2002000638A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
;                     Fusion Proteins and BPI-Derived Peptides
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,527
; FILING DATE: 18-Jan-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/621,803
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael P.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 246:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 813 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: "gelonin"
; SEQUENCE DESCRIPTION: SEQ ID NO: 246:
US-09-765-527-246

Query Match      88.6%; Score 24.8; DB 3; Length 813;
Best Local Similarity 92.9%; Pred. No. 3;
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CACATGTAATAACAAGACTTCATTTTGGC 28
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DB      303 CACAATTAATAACAAGACTTCATTTTGGC 330

RESULT 4
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US-10-127-890-11
; Sequence 11, Application US/10127890
; Publication No. US20030166196A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Studnika, Gary M.
; Carroll, Stephen F.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/127,890
; FILING DATE: 23-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 813 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-127-890-11
Query Match 88.6%; Score 24.8; DB 6; Length 813;
Best Local Similarity 92.9%; Pred. No. 3;
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 CACATGTAACAAACAGACTTCATTTTGGC 28
Db 303 CACAATTAACAAACAGACTTCATTTTGGC 330
RESULT 5
US-10-717-243-11
; Sequence 11, Application US/10717243
; Publication No. US20050054835A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Carroll, Stephen F.
; Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/717,243
; FILING DATE: 18-Nov-2003
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/839,765
; FILING DATE: 15-APR-1997
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 813 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-717-243-11
Query Match 88.6%; Score 24.8; DB 9; Length 813;
Best Local Similarity 92.9%; Pred. No. 3;
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 CACATGTAACAAACAGACTTCATTTTGGC 28
Db 303 CACAATTAACAAACAGACTTCATTTTGGC 330
RESULT 6
US-09-765-527-258
; Sequence 258, Application US/09765527
; Patent No. US20020006638A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; Fusion Proteins and BPI-Derived Peptides
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshhall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
```



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; LOCATION: AA 274-275
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; /note="EagI cloning site."
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; FEATURE:
; NAME/KEY: misc feature
; LOCATION: AA 276-279
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; /note="Ala-Leu-Asp-Pro linking sequence with Asp-Pro cleavage
; site."
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; FEATURE:
; NAME/KEY: misc feature
; LOCATION: AA 280-309
; OTHER INFORMATION: /label= peptide sequence
; /note="BPI-derived peptide."
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; NAME/KEY: misc feature
; LOCATION: residues 993-1011
; OTHER INFORMATION: /label= XhoI
; /note="residues 993-1003 comprise stop codon and XhoI site."
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; SEQUENCE DESCRIPTION: SEQ ID NO: 252:
US-09-765-527-252

Query Match 88.6%; Score 24.8; DB 3; Length 1003;
Best Local Similarity 92.9%; Pred. No. 3.1;
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CACATGTAACAAGACTTCATTGGC 28
Db 434 CACAATTAACAAGACTTCATTGGC 461

RESULT 8
US-09-765-527-250
; Sequence 250, Application US/09765527
; Patent No. US20020006638A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; Fusion Proteins and BPI-Derived Peptides
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/09/765,527
; APPLICATION NUMBER: US/09/765,527
; FILING DATE: 18-Jan-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/621,803
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 250:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1072 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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; NAME/KEY: CDS
; LOCATION: 66..1061
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; FEATURE:
; NAME/KEY: misc feature
; LOCATION: residues 1-65
; OTHER INFORMATION: /label= EcoRI
; /note="residues 1-65 comprise Scori site to beginning of pel
; B."
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; FEATURE:
; NAME/KEY: misc feature
; LOCATION: AA 1-22
; OTHER INFORMATION: /label= pel B
; /note="pel B is the leader sequence from the pectate lyase
; gene of Erwinia caratovora."
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; FEATURE:
; NAME/KEY: misc feature
; LOCATION: AA 23-273
; OTHER INFORMATION: /label= "gelonin"
; /note="gelonin (see U.S. Patent No. 5,416,202)."
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; FEATURE:
; NAME/KEY: misc feature
; LOCATION: AA 274-276
; OTHER INFORMATION: /label= EagI
; /note="EagI cloning site."
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; FEATURE:
; NAME/KEY: misc feature
; LOCATION: AA 277-296
; OTHER INFORMATION: /label= SLT linker
; /note="SLT from shiga-like-toxin gene."
;
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: AA 297-298
; OTHER INFORMATION: /label= FspI/ScaI
; /note="FspI and ScaI cloning sites."
;
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: AA 299-302
; OTHER INFORMATION: /label= cleavage linker
; /note="Ala-Leu-Asp-Pro linking sequence with Asp-Pro cleavage
; site."
;
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: AA 303-332
; OTHER INFORMATION: /label= XhoI
; /note="residues 1062-1072 comprise stop codon and XhoI site."
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 250:
US-09-765-527-250

Query Match 88.6%; Score 24.8; DB 3; Length 1072;
Best Local Similarity 92.9%; Pred. No. 3.2;
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CACATGTAACAAGACTTCATTGGC 28
Db 434 CACAATTAACAAGACTTCATTGGC 461

RESULT 9
US-10-074-596-2
; Sequence 2, Application US/10074596
; Publication No. US2003017633A1
; GENERAL INFORMATION:
; APPLICANT: ROSENBLUM, MICHAEL G.
; APPLICANT: CHEUNG, LAWRENCE
; TITLE OF INVENTION: MODIFIED PROTEINS, DESIGNER TOXINS, AND METHODS OF
; MAKING THEREOF
; FILE REFERENCE: CLFR:007US
```



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; ; CURRENT APPLICATION NUMBER: US/10/074,596
; ; CURRENT FILING DATE: 2002-02-12
; ; PRIOR APPLICATION NUMBER: 60/268,402
; ; PRIOR FILING DATE: 2001-02-12
; ; NUMBER OF SEQ ID NOS: 11
; ; SOFTWARE: Patentin Ver. 2.1
; ; SEQ ID NO 2
; ; LENGTH: 1176
; ; TYPE: DNA
; ; ORGANISM: Gelonium multiflorum
US-10-074-596-2

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Query Match 88.6%; Score 24.8; DB 6; Length 1176;
Best Local Similarity 92.9%; Pred. No. 3.2;
Matches 26: Conservative 0; Mismatches 2; Indels 0

Qy 1 CACATGTA AAAACAAGACTTTCATT TGGC 28
|||||

Db 464 CACATTTAAAACAAGACTTTCATT TGGC 491

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RESULT 10
US-10-964-195-12
; Sequence 12, Application US/10964195
; Publication No. US20050163774A1
; GENERAL INFORMATION:
; APPLICANT: Rosenblum et al.
; TITLE OF INVENTION: Immunotoxins Directed Against c-erbB-2 (HER-2/Neu)
; TITLE OF INVENTION: Related Surface Antigens
; FILE REFERENCE: D5425CIP2
; CURRENT APPLICATION NUMBER: US/10/964,195
; CURRENT FILING DATE: 2004-10-13
; PRIOR APPLICATION NUMBER: US/09/320,156
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: 08/404,499
; PRIOR FILING DATE: 1995-03-17
; NUMBER OF SEQ ID NOS: 14
; SEQ ID NO 12
; LENGTH: 1500
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: nucleotide sequence encoding scFv23-gelonin
; OTHER INFORMATION: immunotoxin
US-10-964-195-12

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Query Match 88.6%; Score 24.8; DB 9; Length 1500;
Best Local Similarity 92.9%; Pred. No. 3.4;
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CACATGTAAAAACAAGACTTCATTTTGGC 28
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Dp 1041 CACAAATTAAAAACAAGACTTCATTTTGGC 1068

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RESULT 11
US-10-074-596-10
; Sequence 10, Application US/10074596
; Publication NO. US20030176331A1
; GENERAL INFORMATION:
; APPLICANT: ROSENBELUM, MICHAEL G.
; APPLICANT: CHEUNG, LAWRENCE
; TITLE OF INVENTION: MODIFIED PROTEINS, DESIGNER TOXINS, AND METHODS OF
; TITLE OF INVENTION: MAKING THEOBF
; FILE REFERENCE: CLFR:007US
; CURRENT APPLICATION NUMBER: US/10/074,596
; CURRENT FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: 60/266,402
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 1527

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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; NAME/KEY: CDS
; LOCATION: (1)..(1521)
US-10-074-596-10

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Query Match      88.6%; Score 24.8; DB 6; Length 1527;
Best Local Similarity 92.9%; Pred. No. 3.4;
Matches 26: Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 1 CACATGTAACCAAGACTTCATTTTGGC 28
|||||
Db 1071 CACAATTAAAAACAAGACTTCATTTTGGC 1098

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RESULT 12
US-11-084-080-25
; Sequence 25, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis J.
; APPLICANT: HELLEDOORN, Koen
; APPLICANT: CIZEAU, Jeannick
; APPLICANT: MACDONALD, Glen Christopher
; APPLICANT: ENTWISTLE, Joycelyn
; APPLICANT: BOSC, Denis Georges
; APPLICANT: GLOVER, Nicholas Ronald
; TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
; TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
; FILE REFERENCE: 10241-44
; CURRENT APPLICATION NUMBER: US/11/084,080
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US 60/554,580
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/630,571
; PRIOR FILING DATE: 2004-11-26
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 25
; LENGTH: 2407
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VB6-845-gelonin
US-11-084-080-25

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Query Match	88.6%	Score 24.8;	DB 10;	Length 2407;
Best Local Similarity	92.9%	Pred. No. 3.7;		
Matches 26: Conservative	0:	Mismatches 2:	Indels 0:	Gaps 0:

QY 1 CACATGTA AAAACAAGACTTCA TTTTGGC 28
||| ||| ||| ||| ||| ||| ||| |||
D6 1127 CACAATTAAAA CAAGACTTCA TTTTGGC 1154

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RESULT 13
US-10-972-079-84211
; Sequence 84211, Application US/10972079
; Publication No. US2005015317A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: ROSENFELD, David
; APPLICANT: KERR, Richard
; APPLICANT: BATES, Stephen
; APPLICANT: HOLM, Tom
; TITLE OF INVENTION: METHODS & SYSTEMS FOR
; TITLE OF INVENTION: LIVESTOCK
; FILE REFERENCE: MM1110-2
; CURRENT APPLICATION NUMBER: US/10972,079

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; CURRENT FILING DATE: 2004-10-22
; PRIOR APPLICATION NUMBER: US 60/514,333
; PRIOR FILING DATE: 2003-10-24
; NUMBER OF SEQ ID NOS: 96631
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 84211
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Chicken 19866894381474_1
US-10-972-079-84211

Query Match 77.1%; Score 21.6; DB 9; Length 600;
Best Local Similarity 85.7%; Pred. No. 63;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 CACATGTAACAAAGACTTCATTTTGGC 28
Db 320 CACTGTGAAGACATGACTTCATTTTGAC 347

RESULT 14
US-10-972-079-84212
; Sequence 84212, Application US/10972079
; Publication No. US20050153317A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: ROSENFELD, David
; APPLICANT: KERR, Richard
; APPLICANT: BATES, Stephen
; APPLICANT: HOLM, Tom
; TITLE OF INVENTION: METHODS & SYSTEMS FOR INFERRING TRAITS TO BREED & MANAGE NON-BEER
; FILE REFERENCE: MW1110-2
; CURRENT APPLICATION NUMBER: US/10/972,079
; PRIOR FILING DATE: 2004-10-22
; PRIOR APPLICATION NUMBER: US 60/514,333
; PRIOR FILING DATE: 2003-10-24
; NUMBER OF SEQ ID NOS: 96631
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 84212
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Chicken 19866894381474_2
US-10-972-079-84212

Query Match 77.1%; Score 21.6; DB 9; Length 600;
Best Local Similarity 85.7%; Pred. No. 63;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 CACATGTAACAAAGACTTCATTTTGGC 28
Db 303 CACTGTGAAGACATGACTTCATTTTGAC 330

RESULT 15
US-10-972-079-84213
; Sequence 84213, Application US/10972079
; Publication No. US20050153317A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: ROSENFELD, David
; APPLICANT: KERR, Richard
; APPLICANT: BATES, Stephen
; APPLICANT: HOLM, Tom
; TITLE OF INVENTION: METHODS & SYSTEMS FOR INFERRING TRAITS TO BREED & MANAGE NON-BEER
; FILE REFERENCE: MW1110-2
; CURRENT APPLICATION NUMBER: US/10/972,079
; PRIOR FILING DATE: 2004-10-22
; PRIOR APPLICATION NUMBER: US 60/514,333
; PRIOR FILING DATE: 2003-10-24

; NUMBER OF SEQ ID NOS: 96631
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 84213
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Chicken 19866894381474_3
US-10-972-079-84213

Query Match 77.1%; Score 21.6; DB 9; Length 600;
Best Local Similarity 85.7%; Pred. No. 63;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 CACATGTAACAAAGACTTCATTTTGGC 28
Db 211 CACTGTGAAGACATGACTTCATTTTGAC 238

Search completed: February 13, 2006, 01:05:13
Job time : 425 secs

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OM nucleic - nucleic search, using sw model

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(without alignments)
118.757 Million cell updates/sec

Title: US-10-717-243-59

Perfect score: 28

Sequence: 1 CACATGTAACAGACTTCATTTCGC 28

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Searched: 6240305 seqs, 449581930 residues

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq*
- 3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq*
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- 8: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq*
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- 11: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq*
- 12: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	19.8	70.7	2229	US-10-750-185-61204
2	19.8	70.7	2229	Sequence 61204, A
3	19.4	69.3	172147	US-10-750-623-61204
4	19.4	69.3	212805	Sequence 22, Appl
5	19.4	69.3	212805	US-11-112-908-22
6	19.4	69.3	1706	US-10-517-151-5
7	19.4	69.3	1720	US-10-131-826A-7
8	19.4	69.3	1770	US-10-750-185-35041
9	18.8	67.1	50	US-10-750-623-35041
10	18.8	67.1	150038	US-11-121-086-23
11	18.6	66.4	2166	US-10-750-185-56714
12	18.6	66.4	2166	Sequence 56714, A
13	18.6	66.4	3829	US-10-821-234-289
14	18.4	65.7	2007	US-10-750-185-59158
15	18.4	65.7	2007	US-10-750-623-59158
16	18.4	64.3	600	US-11-136-527-6304
17	18.4	64.3	894	US-10-750-185-49301
18	18.4	64.3	894	Sequence 49301, A
19	18.4	64.3	1021	US-11-128-061-392
20	18.4	64.3	1021	Sequence 392, Appl
21	18.4	64.3	1021	US-11-128-049-392

c 23	18	64.3	1021	11	US-11-128-049-4034	Sequence 4034, Ap
c 24	18	64.3	1157	7	US-10-750-185-54291	Sequence 54291, A
c 25	18	64.3	1157	7	US-10-750-623-54291	Sequence 54291, A
c 26	18	64.3	1685	7	US-10-750-185-54238	Sequence 54238, A
c 27	18	64.3	1685	7	US-10-750-623-54238	Sequence 54238, A
c 28	18	64.3	1872	7	US-10-750-185-44054	Sequence 44054, A
c 29	18	64.3	1872	7	US-10-750-623-44054	Sequence 44054, A
c 30	17.8	63.6	1748	7	US-11-136-527-2208	Sequence 2208, Ap
c 31	17.8	63.6	1748	7	US-10-689-742-67	Sequence 67, Appl
c 32	17.8	63.6	1837	7	US-10-750-185-59976	Sequence 59976, A
c 33	17.8	63.6	1837	7	US-10-750-623-59976	Sequence 59976, A
c 34	17.8	63.6	16329	11	US-11-150-888-16	Sequence 16, Appl
c 35	17.6	62.9	50	11	US-11-091-018-1	Sequence 1, Appl
c 36	17.6	62.9	274	11	US-11-175-859-88644	Sequence 88644, A
c 37	17.6	62.9	1463	7	US-11-043-752-1038	Sequence 1038, Ap
c 38	17.6	62.9	1463	7	US-10-750-185-50800	Sequence 50800, A
c 39	17.6	62.9	1799	7	US-10-750-623-50800	Sequence 50800, A
c 40	17.6	62.9	1799	7	US-10-750-185-44498	Sequence 44498, A
c 41	17.6	62.9	1958	7	US-10-750-623-44498	Sequence 44498, A
c 42	17.6	62.9	1958	7	US-10-750-185-44527	Sequence 44527, A
c 43	17.6	62.9	2526	11	US-10-750-623-44527	Sequence 44527, A
c 44	17.6	62.9	35100	11	US-11-052-554A-486	Sequence 486, App
c 45	17.6	62.9	60158	11	US-11-127-832-26	Sequence 26, Appl
c 45	17.6	62.9	60158	11	US-11-124-367A-5065	Sequence 5065, Ap

ALIGNMENTS

RESULT 1
US-10-750-185-61204
; Sequence 61204, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 61204
; LENGTH: 2229
; TYPE: DNA
; ORGANISM: Bovine 19866880972028
US-10-750-185-61204
Query Match 70.7%; Score 19.8; DB 7; Length 2229;
Best Local Similarity 91.3%; Pred No. 39;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 6 GTAAACCAAGACTTCATTTCGC 28
Db 1332 GTAAACCAAGACTTCATTTCGC 1354
RESULT 2
US-10-750-623-61204
; Sequence 61204, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David


```
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM11100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61204
; LENGTH: 2229
; TYPE: DNA
; ORGANISM: Bovine 19866880972028
US-10-750-623-61204

Query Match          70.7%; Score 19.8; DB 7; Length 172147;
Best Local Similarity 91.3%; Pred. No. 39;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GTAAACAAGACTTCATTGGC 28
DB 1332 GTAAACAAGACTTCATTGGAC 1354

RESULT 3
US-11-112-908-22
; Sequence 22, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22
; LENGTH: 172147
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-22

Query Match          69.3%; Score 19.4; DB 11; Length 172147;
Best Local Similarity 95.2%; Pred. No. 73;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 AAAACAAGACTTCATTGGC 28
DB 12427 AAAATAAGACTTCATTGGC 12447

RESULT 4
US-11-112-908-19
; Sequence 19, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; CURRENT FILING DATE: 2005-04-22
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; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 19
; LENGTH: 212805
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-19

Query Match          69.3%; Score 19.4; DB 11; Length 212805;
Best Local Similarity 95.2%; Pred. No. 74;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 AAAACAAGACTTCATTGGC 28
DB 173946 AAAATAAGACTTCATTGGC 173966

RESULT 5
US-10-517-151-5
; Sequence 5, Application US/10517151
; Publication No. US20060019252A1
; GENERAL INFORMATION:
; APPLICANT: Nakamura, Yusuke
; APPLICANT: Furukawa, Yoichi
; APPLICANT: Oncotherapy Science, Inc.
; APPLICANT: The University of Tokyo
; TITLE OF INVENTION: Genes and Polypeptides Relating to Hepato cellular or
; TITLE OF INVENTION: Colorectal Carcinoma
; FILE REFERENCE: 082379-000400US
; CURRENT APPLICATION NUMBER: US/10/517,151
; CURRENT FILING DATE: 2004-12-06
; PRIOR APPLICATION NUMBER: US 60/386,985
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: WO PCT/JP03/07070
; PRIOR FILING DATE: 2003-06-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 1706
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (205)..(705)
; OTHER INFORMATION:
US-10-517-151-5

Query Match          67.9%; Score 19; DB 6; Length 1706;
Best Local Similarity 81.5%; Pred. No. 82;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 ACATGTAAACAAGACTTCATTGGC 28
DB 775 ACATGTAAATGCTAAATTCATTGGC 801

RESULT 6
US-10-131-826A-7
; Sequence 7, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
```



```

; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 7
; LENGTH: 1730
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-131-826A-7

Query Match 67.9%; Score 19; DB 7; Length 1730;
Best Local Similarity 81.5%; Pred. No. 82;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 ACATGTAACAAAGACTTCATTTGGC 28
Db 800 ACATGTAATGCTAAATTCATTTGGC 826

RESULT 7
US-10-185-35041/c
; Sequence 35041, Application US/10750185
; Publication No. US200502603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31

; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 35041
; LENGTH: 1770
; TYPE: DNA
; ORGANISM: Bovine
US-10-750-623-35041/c

Query Match 67.9%; Score 19; DB 7; Length 1770;
Best Local Similarity 81.5%; Pred. No. 82;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CACATGTAACAAAGACTTCATTTGG 27
Db 416 CACATGTAACAAAGACTTCATTTGG 390

RESULT 8
US-10-750-623-35041/c
; Sequence 35041, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 35041
; LENGTH: 1770
; TYPE: DNA
; ORGANISM: Bovine
US-10-750-623-35041

Query Match 67.9%; Score 19; DB 7; Length 1770;
Best Local Similarity 81.5%; Pred. No. 82;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CACATGTAACAAAGACTTCATTTGG 27
Db 416 CACATGTAACAAAGACTTCATTTGG 390

RESULT 9
US-11-175-859-30235/c
; Sequence 30235, Application US/11175859
; Publication No. US20060024715A1
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; APPLICANT: Liu, Guoying et al.
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism
; FILE REFERENCE: 3690.1
; CURRENT APPLICATION NUMBER: US/11/175,859
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: US 60/585,352
; PRIOR FILING DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 118251
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 30235
; LENGTH: 50
; TYPE: DNA
; ORGANISM: homo sapien
US-11-175-859-30235
```



```
Query Match          67.1%; Score 18.8; DB 11; Length 50;
Best Local Similarity 83.3%; Pred. No. 80;
Matches 20; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

Qy 1 CACATGTAACCAAGACTTCATTT 24
|||:|||||
Db 29 CACRTGTAACCAACATTTCAATTT 6

```

RESULT 10
US-11-121-086-23
; Sequence 23, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, TIM S.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121.086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 23
; LENGTH: 150038
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-23

```

```
Query Match          67.1%; Score 18.8; DB 11; Length 150038;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 20: Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

	6	G T A A A C A A G A C T T C A T T T T G G	27
Qy			
	136640	G T A A A C A A C A C A C T T C T T T T T G G	136661
Dδ			

```

RESULT 11
US-10-750-185-56714/c
; Sequence 56714, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: WM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 56714
; LENGTH: 2166
; TYPE: DNA
; ORGANISM: Bovine
US-10-750-185-56714

```

Query Match 66.4%; Score 18.6; DB 7; Length 2166;
Best Local Similarity 84.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 ATGTAAACAAGACTTCATTTGGC 28
DB 1814 AAGTGACTAAGACTTCATTTGGC 1790

RESULT 12
US-10-750-623-56714/c

```

? Sequence 56714, Application US/10750623
? Publication No. US20050287531A1
? GENERAL INFORMATION:
? APPLICANT: MMI GENOMICS, INC.
? APPLICANT: DENISE, Sue K.
? APPLICANT: KERR, Richard
? APPLICANT: ROSENFELD, David
? APPLICANT: HOLM, Tom
? APPLICANT: BATES, Stephen
? APPLICANT: FANTIN, Dennis
? TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
? FILE OF INVENTION: MM1100-1
? CURRENT APPLICATION NUMBER: US/10/750,623
? CURRENT FILING DATE: 2003-12-31
? PRIOR APPLICATION NUMBER: US 60/437,482
? PRIOR FILING DATE: 2002-12-31
? NUMBER OF SEQ ID NOS: 64922
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 56714
? LENGTH: 2166
? TYPE: DNA
? ORGANISM: Bovine
? US-10-750-623-56714

```

Query Match	66.4%	Score 18.6;	DB 7;	Length 2166;
Best Local Similarity	84.0%	Pred. No. 1.2e+02;		
Matches 21; Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0;

QY 4 ATGTAAACAAGACTTCATTTGGC 28
 | | | | |
Db 1814 RASTGACTAAGACTTCATTTGGC 1790

```

RESULT 13
US-10-821-234-289/c
; Sequence 289, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462, 047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 289_
; LENGTH: 3829
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-821-234-289

```

Query Match	66.4%	Score 18.6;	DB 7;	Length 3829;
Best Local Similarity	84.0%	Pred. No. 1.2e+02;		
Matches 21: Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0;

Qy		1	CACATGTTAAACAAGACTTTCATTTT	25
Dβ		1194	CTCATTTTAAAAACAAGACTTCAGATT	1170

RESULT 14
US-10-750-185-59158
; Sequence 59158, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:

; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59158
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Bovine 19866881015410
US-10-750-185-59158

Query Match 65.7%; Score 18.4; DB 7; Length 2007;
Best Local Similarity 78.6%; Pred. No. 1.4e+02;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CACATGTAAACAAGACTTCATTTGGC 28
||| ||||| ||||| ||||| |||||
Db 1535 CATGTGGAACAACAAAGCTTCATTCCTGGC 1562

RESULT 15
US-10-750-623-59158
; Sequence 59158, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59158
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Bovine 19866881015410
US-10-750-623-59158

Query Match 65.7%; Score 18.4; DB 7; Length 2007;
Best Local Similarity 78.6%; Pred. No. 1.4e+02;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CACATGTAAACAAGACTTCATTTGGC 28
||| ||||| ||||| ||||| |||||
Db 1535 CATGTGGAACAACAAAGCTTCATTCCTGGC 1562

Search completed: February 13, 2006, 01:08:51
Job time : 213 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 10, 2006, 09:56:49 ; Search time 136.614 Seconds
(without alignments)
807.265 Million cell updates/sec

Title: US-10-717-243-101

Perfect score: 1277

Sequence: 1 GLDVTVSFTSGATVITYVNF.....AVDQVKP KIALLKFDVKDPK 251

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1277	100.0	251	2	AAR63914
2	1273	99.7	251	2	AAR63912
3	1269	99.4	251	2	AAR63903
4	1269	99.4	251	2	AAR63915
5	1269	99.4	251	8	ADG63044
6	1269	99.4	316	5	ABG71551
7	1269	99.4	498	9	ABEB68722
8	1269	99.4	507	5	ABG71552
9	1266	99.1	293	2	AAW29300
10	1266	99.1	309	2	AAW29303
11	1266	99.1	332	2	AAW29294
12	1264	99.0	251	2	AAR63923
13	1261	98.7	251	2	AAR63921
14	1261	98.7	251	2	AAR63918
15	1261	98.7	251	2	AAR63920
16	1261	98.7	251	2	AAR63919
17	1261	98.7	251	2	AAR63924
18	1260	98.7	251	2	AAR63922
19	1260	98.7	251	2	AAR63916
20	1260	98.7	251	2	AAR63917
21	1257	98.4	251	2	AAR74177
22	1251	98.0	251	2	AAR37291
23	1235.5	96.8	258	2	AAR22227
24	1201	94.0	506	9	ABEB68720

25	1171	91.7	235	2	AAR63913
26	348	27.3	263	2	AAR63905
27	348	27.3	263	2	AAR74179
28	348	27.3	263	8	ADG63043
29	347	27.2	565	1	AAP50166
30	347	27.2	565	4	AAG78300
31	347	27.2	574	1	AAP70325
32	346	27.1	267	2	AAR30722
33	346	27.1	267	2	AAR37290
34	346	27.1	267	2	AAR63902
35	346	27.1	267	3	ABAB19265
36	346	27.1	267	7	ADC24288
37	346	27.1	268	2	AAR39570
38	346	27.1	290	2	AAW21699
39	346	27.1	290	2	AAW25136
40	346	27.1	332	1	AAP70097
41	346	27.1	332	1	AAP70838
42	346	27.1	332	1	AAP95639
43	346	27.1	554	2	AAR70827
44	346	27.1	562	1	AAP90079
45	346	27.1	565	4	AAG78304

ALIGNMENTS

RESULT 1

ID	AAR63914	standard; protein; 251 AA.
XX	AC	
XX	AAR63914;	
DT	25-MAR-2003	(revised)
DT	27-JUL-1995	(first entry)
XX	Type I RIP	gelonin analog Gel (A44/A50) .
XX	Type I	ribosome-inactivating proteins; RIPs; gelonin;
KW	cytotoxic therapeutic agents;	autoimmune disease; cancer;
KW	graft-versus-host disease.	
XX	Gelonium multiflorum.	
OS	Gelonium multiflorum.	
PN	WO9426910-A1.	
XX	24-NOV-1994.	
XX	12-MAY-1994;	94WO-US005348.
PR	12-MAY-1993;	93US-00064691.
XX	(XOMA)	XOMA CORP.
XX	Better MD,	Carroll SP, Studnicka GM;
XX	WPI,	1995-006804/01.
XX	Polynucleotide(s)	encoding type I ribosome-inactivating proteins - which
PT	are suitable for use as	components of cytotoxic therapeutic agents.
XX	Example 3;	Page 181-182; 221pp; English.

AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating protein (RIP) gelonin, one of the nine RIPs described in AAR63903-R63911. RIPs are key components of cytotoxic therapeutic agents (CTAs), which include gene fusion products and immunocjugates. CTAs may be used to selectively eliminate any cell type to which a RIP component is targeted, by the specific binding capacity of the second component of the agent. They can be used in the treatment of diseases where the elimination of a particular cell type is desired, such as autoimmune disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to correct PN field.)


```
SQ Sequence 251 AA;
Query Match 100.0%; Score 1277; DB 2; Length 251;
Best Local Similarity 100.0%; Pred. No. 4.9e-120;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLDVSFSTKGTATYYVNFNLRLVRLKPGNSHGIPLLRKADDPGKAFVLVALSNDN 60
DB 1 GLDVSFSTKGTATYYVNFNLRLVRLKPGNSHGIPLLRKADDPGKAFVLVALSNDN 60
QY 61 GOLAEIAIDVTSVYVVGQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGSGYPSLEGEK 120
DB 61 GOLAEIAIDVTSVYVVGQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGSGYPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQVSEAAARFTFIENQIRNN 180
QY 181 FQORIRPANNTISLENKWKGLSFQIRTSANGMFSSEAVELERANGKYYVTVAVDQVKPKI 240
DB 181 FQORIRPANNTISLENKWKGLSFQIRTSANGMFSSEAVELERANGKYYVTVAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 2
AAR63912
ID AAR63912 standard; protein; 251 AA.
XX
AC AAR63912;
XX
DT 25-MAR-2003 (revised)
DT 27-JUL-1995 (first entry)
DE Type I RIP gelonin analog Gel (A50/C44).
XX
XX Type I ribosome-inactivating proteins; RIPs; gelonin;
KW cytotoxic therapeutic agents; autoimmune disease; cancer;
KW graft-versus-host disease.
OS Gelonium multiflorum.
XX
XX WO9426910-A1.
XX
XX 24-NOV-1994.
XX
XX 12-MAY-1994; 94WO-US005348.
XX
XX 12-MAY-1993; 93US-00064691.
XX (XOMA ) XOMA CORP.
XX
XX Better MD, Carroll SF, Studnicka GM;
XX WPI; 1995-006804/01.
XX
XX Polynucleotide(s) encoding type I ribosome-inactivating proteins - which
XX are suitable for use as components of cytotoxic therapeutic agents.
XX
XX Example 3; Page 179-180; 221pp; English.
XX
XX AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating
XX protein (RIP) gelonin, one of the nine RIPs described in AAR63903-R63911.
XX R63912-R63924 are key components of cytotoxic therapeutic agents (CTAs), which
XX include gene fusion products and immunocjugates. CTAs may be used to
XX selectively eliminate any cell type to which a RIP component is
XX targeted, by the specific binding capacity of the second component of
XX the agent. They can be used in the treatment of diseases where the
XX elimination of a particular cell type is desired, such as autoimmune
XX disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to
XX correct PN field.)

XX SQ Sequence 251 AA;
Query Match 99.7%; Score 1273; DB 2; Length 251;
Best Local Similarity 99.6%; Pred. No. 1.2e-119;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLDVSFSTKGTATYYVNFNLRLVRLKPGNSHGIPLLRKADDPGKAFVLVALSNDN 60
DB 1 GLDVSFSTKGTATYYVNFNLRLVRLKPGNSHGIPLLRKADDPGKAFVLVALSNDN 60
QY 61 GOLAEIAIDVTSVYVVGQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGSGYPSLEGEK 120
DB 61 GOLAEIAIDVTSVYVVGQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGSGYPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQVSEAAARFTFIENQIRNN 180
QY 181 FQORIRPANNTISLENKWKGLSFQIRTSANGMFSSEAVELERANGKYYVTVAVDQVKPKI 240
DB 181 FQORIRPANNTISLENKWKGLSFQIRTSANGMFSSEAVELERANGKYYVTVAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 3
AAR63903
ID AAR63903 standard; protein; 251 AA.
XX
AC AAR63903;
XX
DT 25-MAR-2003 (revised)
DT 27-JUL-1995 (first entry)
DE Type I ribosome-inactivating protein gelonin.
XX
XX Type I ribosome-inactivating proteins; RIPs; gelonin;
KW cytotoxic therapeutic agents; autoimmune disease; cancer;
KW graft-versus-host disease.
OS Gelonium multiflorum.
XX
XX WO9426910-A1.
XX
XX 24-NOV-1994.
XX
XX 12-MAY-1994; 94WO-US005348.
XX
XX 12-MAY-1993; 93US-00064691.
XX (XOMA ) XOMA CORP.
XX
XX Better MD, Carroll SF, Studnicka GM;
XX WPI; 1995-006804/01.
XX
XX Polynucleotide(s) encoding type I ribosome-inactivating proteins - which
XX are suitable for use as components of cytotoxic therapeutic agents.
XX
XX Example 1; Fig 1; 221pp; English.
XX
XX AAR63903 encodes AAR63903 type I ribosome-inactivating protein (RIP)
XX gelonin, one of the nine RIPs described in AAR63903-R63911. RIPs are key
XX components of cytotoxic therapeutic agents (CTAs), which include gene
XX fusion products and immunocjugates. CTAs may be used to selectively
XX eliminate any cell type to which a RIP component is targeted, by the
XX specific binding capacity of the second component of the agent. They can
XX be used in the treatment of diseases where the elimination of a
XX particular cell type is desired, such as autoimmune disease, cancer and
```


CC graft-versus-host disease. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 251 AA;

Query Match 99.4%; Score 1269; DB 2; Length 251;
 Best Local Similarity 99.2%; Pred. No. 3.1e-119; Indels 0; Gaps 0;
 Matches 249; Conservative 0; Mismatches 2;
 QY 1 GLDVSFSTKGATYYVNFNLRLVKLPKPGNSHGIPLLRKKADDPGKAPVLVALSNDN 60
 DB 1 GLDVSFSTKGATYYVNFNLRLVKLPKPGNSHGIPLLRKKADDPGKAPVLVALSNDN 60
 QY 61 QQLAEIAIDVTSVYVVGQVNRNSYFFPKDAPDAAYEGLFKNTIKTRLHFGSGYPSLEGEK 120
 DB 61 QQLAEIAIDVTSVYVVGQVNRNSYFFPKDAPDAAYEGLFKNTIKTRLHFGSGYPSLEGEK 120
 QY 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTETIASLLVVIQMVSEARPTFIENQIRNN 180
 DB 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTETIASLLVVIQMVSEARPTFIENQIRNN 180
 QY 181 FQQRIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
 DB 181 FQQRIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
 QY 241 ALLKFVDKDPK 251
 DB 241 ALLKFVDKDPK 251

RESULT 4

AA63915
 ID AAR63915 standard; protein; 251 AA.

XX AAR63915;

XX 25-MAR-2003 (revised)
 DT 27-JUL-1995 (first entry)

XX Type I RIP gelonin analog Gel (C10/A44/A50).

XX Type I ribosome-inactivating proteins; RIPS; gelonin;
 KW cytotoxic therapeutic agents; autoimmune disease; cancer;
 KW graft-versus-host disease.

XX Gelonium multiflorum.

XX WO9426910-A1.

XX 24-NOV-1994.

XX 12-MAY-1994; 94WO-US005348.

XX 12-MAY-1993; 93US-00064691.

XX (XOMA) XOMA CORP.

XX Better MD, Carroll SF, Studnicka GW;

XX WPI; 1995-006804/01.

XX Polynucleotide(s) encoding type I ribosome-inactivating proteins - which
 PT are suitable for use as components of cytotoxic therapeutic agents.

XX Example 3; Page 189-190; 221pp; English.

XX AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating
 CC protein (RIP) gelonin, one of the nine RIPS described in AAR63903-R63911.
 CC RIPS are key components of cytotoxic therapeutic agents (CTAs), which
 CC include gene fusion products and immunoconjugates. CTAs may be used to
 CC selectively eliminate any cell type to which a RIP component is
 CC targeted, by the specific binding capacity of the second component of
 CC the agent. They can be used in the treatment of diseases where the
 CC elimination of a particular cell type is desired, such as autoimmune

CC disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to
 CC correct PN field.)

SQ Sequence 251 AA;

Query Match 99.4%; Score 1269; DB 2; Length 251;
 Best Local Similarity 99.6%; Pred. No. 3.1e-119; Indels 0; Gaps 0;
 Matches 250; Conservative 0; Mismatches 1;
 QY 1 GLDVSFSTKGATYYVNFNLRLVKLPKPGNSHGIPLLRKKADDPGKAPVLVALSNDN 60
 DB 1 GLDVSFSTKGATYYVNFNLRLVKLPKPGNSHGIPLLRKKADDPGKAPVLVALSNDN 60
 QY 61 QQLAEIAIDVTSVYVVGQVNRNSYFFPKDAPDAAYEGLFKNTIKTRLHFGSGYPSLEGEK 120
 DB 61 QQLAEIAIDVTSVYVVGQVNRNSYFFPKDAPDAAYEGLFKNTIKTRLHFGSGYPSLEGEK 120
 QY 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTETIASLLVVIQMVSEARPTFIENQIRNN 180
 DB 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTETIASLLVVIQMVSEARPTFIENQIRNN 180
 QY 181 FQQRIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
 DB 181 FQQRIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
 QY 241 ALLKFVDKDPK 251
 DB 241 ALLKFVDKDPK 251

RESULT 5

ADG63044

ID ADG63044 standard; protein; 251 AA.

XX ADG63044;

XX 11-MAR-2004 (first entry)

XX Gelonium anti-HIV protein 31kDa (GAP31).

XX anti-HIV; cytostatic; peptide therapy; anti-tumour; antiviral; MAP30;
 KW GAP31; HIV; tumour; gelonium anti-HIV protein 31kDa.

XX Gelonium multiflorum.

XX US6652861-B1.

XX 25-NOV-2003.

XX 25-AUG-2000; 2000US-00645603.

XX 26-AUG-1999; 99US-0150885P.

XX (UYNY) UNIV NEW YORK STATE.

XX Lee-Huang S;

XX WPI; 2004-050519/05.

XX New MAP30 or GAP31 peptides or polypeptides having an anti-tumor and
 PT antiviral activity, useful for treating human immunodeficiency virus
 PT infection or tumor.

XX Example 1; SEQ ID NO 2; 22pp; English.

XX The invention describes an isolated peptide or polypeptide having an anti
 CC -tumor and antiviral activity. Also described is a composition
 CC comprising the isolated peptide or polypeptide, and a carrier, excipient
 CC or auxiliary agent. Specifically claimed are MAP30 or GAP31 peptides or
 CC polypeptides. The peptide or polypeptide is useful for treating HIV
 CC infection, and tumour. This is the amino acid sequence of gelonium anti-
 CC HIV protein 30kDa (MAP30).


```
SQ Sequence 251 AA;
Query Match 99.4%; Score 1269; DB 8; Length 251;
Best Local Similarity 99.2%; Pred. No. 3.1e-119;
Matches 249; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GLDTVSFSTKGATYTYVNFNLRLVKLPKGNHSHGIPLLRKKADDPKAPVLVLSNDN 60
DB 1 GLDTVSFSTKGATYTYVNFNLRLVKLPKGNHSHGIPLLRKKADDPKAPVLVLSNDN 60

QY 61 QQLAEIAIDVTSVYVVGQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLGEK 120
DB 61 QQLAEIAIDVTSVYVVGQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLGEK 120

QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTAISLLVVIQWVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTAISLLVVIQWVSEAAARFTFIENQIRNN 180

QY 181 FQORIRPANNTISLENKWKGLSFQIRTSANGMPSEAVELERANGKKYVTVAVDQVKPKI 240
DB 181 FQORIRPANNTISLENKWKGLSFQIRTSANGMPSEAVELERANGKKYVTVAVDQVKPKI 240

QY 241 ALLKFPVDKDPK 251
DB 241 ALLKFPVDKDPK 251

RESULT 6
ABG71551
ID ABG71551 standard; protein; 316 AA.
XX ABG71551;
AC ABG71551;
XX
DT 08-JAN-2003 (first entry)
XX
DE G. multiflorum recombinant gelonin (rGel) toxin.
XX
KW Modified protein; reduced antigenicity; modified toxin; gelonin;
KW designer toxin; immunotoxin; proteinaceous compound; cancer;
KW microbial pathogenesis; acquired immunodeficiency syndrome; AIDS;
KW autoimmune disease; hyperproliferative disorder; leukaemia; arthritis;
KW inflammatory disease; cardiovascular disease; diabetes;
KW pathogenic disease; cytostatic; antiarthritic; antiinflammatory;
KW cardiant; antidiabetic; virucide; protozoacide; fungicide; antibacterial;
KW recombinant gelonin; rGel.
XX
OS Gelonium multiflorum.
XX
FN WO200269886-A2.
XX
PD 12-SEP-2002.
XX
PF 12-FEB-2002; 2002WO-US004195.
XX
PR 12-FEB-2001; 2001US-0268402P.
XX
PA (RERE-) RES DEV FOUND.
XX
PI Rosenblum MG, Cheung L;
XX
DR WPI, 2002-750431/81.
DR N-P5DB; ABS56021.
XX
PT Generating a modified protein with reduced antigenicity for treating
PT cancer, AIDS, autoimmune diseases, comprises identifying a protein region
PT antigenic in the first subject using antiserum from either the first or a
PT second subject.
XX
PS Claim 63; Page 169-170; 176pp; English.
XX
CC The present invention relates to a method of generating a modified
CC protein with reduced antigenicity while maintaining its biological
CC activity. The method comprises identifying a region of the protein that
is antigenic in a first subject using antiserum from either the first
subject or a second subject of the same species as the first subject. In
particular the invention discloses modified toxin compounds, for example
gelonin toxin derived from Gelonium multiflorum, that are truncated
and/or possess reduced antigenicity. Such designer toxins have
therapeutic, diagnostic, and preventative benefits, particularly as
immunotoxins. The method of the invention is useful for generating
proteinaceous compounds with less antigenicity. The immunotoxin and
gelonin toxin are useful for treating cancer, e.g. prostate, lung, brain,
skin, liver, breast, lymphoid, stomach, testicular, ovarian, pancreatic,
bone, bone marrow, head and neck, cervical, oesophagus, eye, gall
bladder, kidney, adrenal glands, heart, colon, or blood cancer. The
compositions of the invention are also useful for treating microbial
pathogenesis, acquired immunodeficiency syndrome (AIDS), autoimmune
diseases, hyperproliferative disorders including cancer, leukaemias,
arthritis, inflammatory diseases, cardiovascular diseases, pathogenic
diseases, and diabetes. The method provides less antigenic proteins,
peptides and polypeptides, which are more effective than prior art. The
present sequence represents G. multiflorum recombinant gelonin (rGel)
XX
SQ Sequence 316 AA;
Query Match 99.4%; Score 1269; DB 5; Length 316;
Best Local Similarity 99.2%; Pred. No. 4.3e-119;
Matches 249; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GLDTVSFSTKGATYTYVNFNLRLVKLPKGNHSHGIPLLRKKADDPKAPVLVLSNDN 60
DB 47 GLDTVSFSTKGATYTYVNFNLRLVKLPKGNHSHGIPLLRKKADDPKAPVLVLSNDN 106

QY 61 QQLAEIAIDVTSVYVVGQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLGEK 120
DB 107 QQLAEIAIDVTSVYVVGQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLGEK 166

QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTAISLLVVIQWVSEAAARFTFIENQIRNN 180
DB 167 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTAISLLVVIQWVSEAAARFTFIENQIRNN 226

QY 181 FQORIRPANNTISLENKWKGLSFQIRTSANGMPSEAVELERANGKKYVTVAVDQVKPKI 240
DB 227 FQORIRPANNTISLENKWKGLSFQIRTSANGMPSEAVELERANGKKYVTVAVDQVKPKI 286

QY 241 ALLKFPVDKDPK 251
DB 287 ALLKFPVDKDPK 297

RESULT 7
AEB68722
ID AEB68722 standard; protein; 498 AA.
XX AEB68722;
AC AEB68722;
XX
DT 06-OCT-2005 (first entry)
XX
DE scFv23-gelonin immunotoxin amino acid sequence SEQ ID NO:13.
XX
KW antibody engineering; c-erbB-2 protein; toxin; gelonin; cytostatic;
KW immunotoxin; neoplasm.
XX
OS Synthetic.
XX
FN US2005163774-A1.
XX
PD 28-JUL-2005.
XX
PF 13-OCT-2004; 2004US-00964195.
XX
PR 10-APR-1992; 92US-00867728.
PR 09-DEC-1993; 93US-00164638.
PR 02-SEP-1994; 94US-00300082.
PR 17-MAR-1995; 95US-00404499.
PR 26-MAY-1999; 99US-00320156.
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XX (RERE-) RES DEV FOUND.
XX Rosenblum M, Shawver LK;
XX WPI; 2005-561813/57.
XX N-PSDB; ABB68721.
XX New immunotoxins directed against c-erbB-2 related surface antigens,
XX useful for treating neoplastic diseases, e.g. carcinoma or
XX adenocarcinoma.
XX Disclosure; SEQ ID NO 13; 60pp; English.
XX The invention relates to a composition comprising a conjugate of an
XX antibody exhibiting binding specificity for an extracellular epitope of c
XX -erbB-2 protein and a plant derived toxin, where the toxin is
XX pharmacologically effective against neoplastic cells and is selected from
XX gelonin, full length recombinant gelonin, functional gelonin fragments or
XX functional gelonin derivatives. Also described is a pharmaceutical
XX composition comprising the composition above and a pharmaceutical
XX vehicle. For treating neoplastic diseases, e.g. human mammary carcinomas,
XX human ovarian carcinomas, lung carcinomas, gastric tumors, salivary gland
XX adenocarcinomas, or colon adenocarcinomas. The present sequence
XX represents a scFv23-gelonin amino acid sequence, which is used in an
XX example from the present invention.
XX Sequence 498 AA;
XX
XX Query Match 99.4%; Score 1269; DB 9; Length 498;
XX Best Local Similarity 99.2%; Pred. No. 8.2e-119;
XX Matches 249; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1 GLDTVSFSTKGATVITYVNFNLRLVKLPKGNHSHGIPLLRKADDPKAFVLVALSNDN 60
XX 247 GLDTVSFSTKGATVITYVNFNLRLVKLPKGNHSHGIPLLRKADDPKAFVLVALSNDN 306
XX
XX 61 GQLAEIAIDVTSVYVGVQVNRNSYFFPKADPAAYEGLFKNTIKTRLHFGSGYPSLEGEK 120
XX 307 GQLAEIAIDVTSVYVGVQVNRNSYFFPKADPAAYEGLFKNTIKTRLHFGSGYPSLEGEK 366
XX
XX 121 AYRTETDLGIEPLRIGIKLDAENADNYKPTAISLLVVIQWVSEARFTFIENQIRNN 180
XX 367 AYRTETDLGIEPLRIGIKLDAENADNYKPTAISLLVVIQWVSEARFTFIENQIRNN 426
XX
XX 181 FQQRIRPANNTISLENKWKLSFOIRTSGANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
XX 427 FQQRIRPANNTISLENKWKLSFOIRTSGANGMFSEAVELERANGKYYVTVAVDQVKPKI 486
XX
XX 241 ALLKFVDKDPK 251
XX 487 ALLKFVDKDPK 497
XX
XX RESULT 8
XX ABG71552
XX ID ABG71552 standard; protein; 507 AA.
XX
XX AC ABG71552;
XX
XX DT 08-JAN-2003 (first entry)
XX
XX DE Murine scfWML/G. multiflorum rGel fusion protein.
XX
XX KW Modified protein; reduced antigenicity; modified toxin; gelonin;
XX designer toxin; immunotoxin; proteinaceous compound; cancer;
XX microbial pathogenesis; acquired immunodeficiency syndrome; AIDS;
XX autoimmune disease; hyperproliferative disorder; leukaemia; arthritis;
XX inflammatory disease; cardiovascular disease; diabetes;
XX pathogenic disease; cytostatic; antiarthritic; antiinflammatory;
XX cadiant; antidiabetic; virucide; protozoacide; fungicide; antibacterial;
XX murine; single-chain ZME-018 antibody; recombinant gelonin; rGel;
XX scfWML/rGel; mutant; mutetin.

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XX Mus sp.
XX Gelonium multiflorum.
XX Synthetic.
XX Chimeric.
XX W0200269886-A2.
XX 12-SEP-2002.
XX 12-FEB-2002; 2002WO-US004195.
XX 12-FEB-2001; 2001US-0268402P.
XX (RERE-) RES DEV FOUND.
XX Rosenblum MG, Cheung L;
XX WPI; 2002-750431/81.
XX N-PSDB; ABS56029.
XX Generating a modified protein with reduced antigenicity for treating
XX cancer, AIDS, autoimmune diseases, comprises identifying a protein region
XX antigenic in the first subject using antiserum from either the first or a
XX second subject.
XX Disclosure; Page 174-176; 176pp; English.
XX The present invention relates to a method of generating a modified
XX protein with reduced antigenicity while maintaining its biological
XX activity. The method comprises identifying a region of the protein that
XX is antigenic in a first subject using antiserum from either the first
XX subject or a second subject of the same species as the first subject. In
XX particular the invention discloses modified toxin compounds, for example
XX gelonin toxin derived from Gelonium multiflorum, that are truncated
XX and/or possess reduced antigenicity. Such designer toxins have
XX therapeutic, diagnostic, and preventative benefits, particularly as
XX immunotoxins. The method of the invention is useful for generating
XX proteinaceous compounds with less antigenicity. The immunotoxin and
XX gelonin toxin are useful for treating cancer, e.g. prostate, lung, brain,
XX skin, liver, breast, lymphoid, stomach, testicular, ovarian, pancreatic,
XX bone, bone marrow, head and neck, cervical, oesophagus, eye, gall
XX bladder, kidney, adrenal glands, heart, colon, or blood cancer. The
XX compositions of the invention are also useful for treating microbial
XX pathogenesis, acquired immunodeficiency syndrome (AIDS), autoimmune
XX diseases, hyperproliferative disorders including cancer, leukaemias,
XX arthritis, inflammatory diseases, cardiovascular diseases, pathogenic
XX diseases, and diabetes. The method provides less antigenic proteins, the
XX peptides and polypeptides, which are more effective than prior art. The
XX present sequence represents murine single-chain ZME-018 antibody/G.
XX multiflorum recombinant gelonin (rGel) (scfWML/rGel) fusion protein
XX Sequence 507 AA;
XX
XX Query Match 99.4%; Score 1269; DB 5; Length 507;
XX Best Local Similarity 99.2%; Pred. No. 8.4e-119;
XX Matches 249; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1 GLDTVSFSTKGATVITYVNFNLRLVKLPKGNHSHGIPLLRKADDPKAFVLVALSNDN 60
XX 257 GLDTVSFSTKGATVITYVNFNLRLVKLPKGNHSHGIPLLRKADDPKAFVLVALSNDN 316
XX
XX 61 GQLAEIAIDVTSVYVGVQVNRNSYFFPKADPAAYEGLFKNTIKTRLHFGSGYPSLEGEK 120
XX 317 GQLAEIAIDVTSVYVGVQVNRNSYFFPKADPAAYEGLFKNTIKTRLHFGSGYPSLEGEK 376
XX
XX 121 AYRTETDLGIEPLRIGIKLDAENADNYKPTAISLLVVIQWVSEARFTFIENQIRNN 180
XX 377 AYRTETDLGIEPLRIGIKLDAENADNYKPTAISLLVVIQWVSEARFTFIENQIRNN 436
XX
XX 181 FQQRIRPANNTISLENKWKLSFOIRTSGANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
XX 437 FQQRIRPANNTISLENKWKLSFOIRTSGANGMFSEAVELERANGKYYVTVAVDQVKPKI 496

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Qy      241 ALLKFDVDDPK 251
Db      497 ALLKFDVDDPK 507

RESULT 9
AAW29300
ID      AAW29300 standard; protein; 293 AA.
XX
AC      AAW29300;
XX
DT      20-APR-1998 (first entry)
XX
DE      BPI peptide fusion protein PING3797 vector construct protein.
XX
KW      Bactericidal/permeability increasing peptide; BPI; fusion protein;
KW      bacterial infection; fungal infection; endotoxin; heparin; angiogenesis;
KW      fungicidal; recombinant DNA; vector.
XX
OS      Synthetic.
OS      Pectobacterium carotovorum.
OS      Homo sapiens.
OS      Chimeric.
XX
FN      WO9735009-A1.
XX
XX      25-SEP-1997.
XX
XX      18-MAR-1997; 97WO-US005287.
XX
XX      22-MAR-1996; 96US-00621803.
XX
XX      (XOMA ) XOMA CORP.
XX
PI      Better MD;
XX
DR      WPI; 1997-480215/44.
DR      N-PSDB; AAT86336.
XX
XX      Recombinant production of bactericidal/permeability increasing protein -
XX      by expression as a fusion protein in microbial host cells, then cleaving
XX      the BPI peptide from the carrier.
XX
XX      Example 1; Page 160-161; 186pp; English.
XX
XX      A new recombinant DNA vector construct has been developed which encodes a
XX      fusion protein and is suitable for introduction into a bacterial host.
XX      The vector comprises: (a) DNA encoding at least one cationic
XX      bactericidal/permeability increasing peptide (BPI); (b) DNA encoding a
XX      carrier protein, and (c) DNA encoding an amino acid (aa) cleavage site
XX      located between (a) and (b). The present sequence represents the protein
XX      from the PING3797 vector construct which codes for a BPI fusion protein.
XX      The peptides have many uses including the treatment of bacterial and
XX      fungal infections. BPI peptides also bind to endotoxins and heparin,
XX      neutralising their effects. The peptides have further been shown to
XX      inhibit angiogenesis (partly due to heparin-binding activity). The fusion
XX      proteins have been found to be expressed in large amounts without
XX      significant proteolysis, and in some cases are actually secreted from the
XX      host cells. This allows the indirect production of anti-microbial BPI
XX      peptides in microbial hosts
XX
XX      Sequence 293 AA;
XX
Query Match          99.1%; Score 1266; DB 2; Length 293;
Best Local Similarity 98.8%; Pred. No. 7, 8e-119;
Matches 248; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy      1 GLDVSFSTKATYTYNFMNLRVKKPGNSHGIPLLRKKADDPKAFVVALSNDN 60
Db      23 GLDVSFSTKATYTYNFMNLRVKKPGNSHGIPLLRKKADDPKAFVVALSNDN 82
Qy      61 GQLAEIAIDVTSVYVGVQVNRYSFFKADPAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120

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Query Match 99.1%; Score 1266; DB 2; Length 309;
Best Local Similarity 98.8%; Pred. No. 8.4e-119;
Matches 248; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 GLDTVSSTKATYITVYVFNELRVKLPKGNHSHGIPLLRKKADDPKAPVLVALSNDN 60
DB 23 GLDTVSSTKATYITVYVFNELRVKLPKGNHSHGIPLLRKKADDPKAPVLVALSNDN 82
QY 61 GOLAEIAIDVTSVYVVGQVNRNSYFFPKADPAAYEGLFKNTIKTRLHFGGTSYPSLEGEK 120
DB 83 GOLAEIAIDVTSVYVVGQVNRNSYFFPKADPAAYEGLFKNTIKTRLHFGGTSYPSLEGEK 142
QY 121 AYRETTDLGIEPLRIGIKLDENAIDNYKPTETIASLLVVIQWVSEAAARFTFIENQIRNN 180
DB 143 AYRETTDLGIEPLRIGIKLDENAIDNYKPTETIASLLVVIQWVSEAAARFTFIENQIRNN 202
QY 181 FQQRIRPANNTISLENKWKGLSFQIRTSANGMSEAVELERANGKYYVTVAVDQVKPKI 240
DB 203 FQQRIRPANNTISLENKWKGLSFQIRTSANGMSEAVELERANGKYYVTVAVDQVKPKI 262
QY 241 ALLKFVDKDPK 251
DB 263 ALLKFVDKDPK 273

RESULT 11

AAW29294
ID AAW29294 standard; protein; 332 AA.
XX AAW29294;
AC AAW29294;
XX XX
XX 20-APR-1998 (first entry)
XX BPI peptide fusion protein PING3793 vector construct protein.
XX Bactericidal/permeability increasing peptide; BPI; fusion protein;
KW bacterial infection; fungal infection; endotoxin; heparin; angiogenesis;
KW fungicidal; recombinant DNA; vector.
XX Synthetic.
OS Pectobacterium carotovorum.
OS Homo sapiens.
OS Chimeric.
XX XX
XX WO9735009-A1.
XX XX
XX 25-SEP-1997.
XX 18-MAR-1997; 97WO-US005287.
XX 22-MAR-1996; 96US-00621803.
XX (XOMA) XOMA CORP.
XX Better MD;
XX WPI; 1997-480215/44.
XX N-PSDB; AAT86332.
XX Recombinant production of bactericidal/permeability increasing protein -
FT by expression as a fusion protein in microbial host cells, then cleaving
FT the BPI peptide from the carrier.
XX Example 1; Page 148-150; 186pp; English.
XX A new recombinant DNA vector construct has been developed which encodes a
CC fusion protein and is suitable for introduction into a bacterial host.
CC The vector comprises: (a) DNA encoding at least one cationic
CC bactericidal/permeability increasing peptide (BPI); (b) DNA encoding a
CC carrier protein; and (c) DNA encoding an amino acid (aa) cleavage site
CC located between (a) and (b). The present sequence represents the protein
CC from the PING3793 vector construct which codes for a BPI fusion protein.

CC The peptides have many uses including the treatment of bacterial and
CC fungal infections. BPI peptides also bind to endotoxins and heparin,
CC neutralizing their effects. The peptides have further been shown to
CC inhibit angiogenesis (partly due to heparin-binding activity). The fusion
CC proteins have been found to be expressed in large amounts without
CC significant proteolysis, and in some cases are actually secreted from the
CC host cells. This allows the indirect production of anti-microbial BPI
CC peptides in microbial hosts
XX XX
SQ Sequence 332 AA;

Query Match 99.1%; Score 1266; DB 2; Length 332;
Best Local Similarity 98.8%; Pred. No. 9.3e-119;
Matches 248; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 GLDTVSSTKATYITVYVFNELRVKLPKGNHSHGIPLLRKKADDPKAPVLVALSNDN 60
DB 23 GLDTVSSTKATYITVYVFNELRVKLPKGNHSHGIPLLRKKADDPKAPVLVALSNDN 82
QY 61 GOLAEIAIDVTSVYVVGQVNRNSYFFPKADPAAYEGLFKNTIKTRLHFGGTSYPSLEGEK 120
DB 83 GOLAEIAIDVTSVYVVGQVNRNSYFFPKADPAAYEGLFKNTIKTRLHFGGTSYPSLEGEK 142
QY 121 AYRETTDLGIEPLRIGIKLDENAIDNYKPTETIASLLVVIQWVSEAAARFTFIENQIRNN 180
DB 143 AYRETTDLGIEPLRIGIKLDENAIDNYKPTETIASLLVVIQWVSEAAARFTFIENQIRNN 202
QY 181 FQQRIRPANNTISLENKWKGLSFQIRTSANGMSEAVELERANGKYYVTVAVDQVKPKI 240
DB 203 FQQRIRPANNTISLENKWKGLSFQIRTSANGMSEAVELERANGKYYVTVAVDQVKPKI 262
QY 241 ALLKFVDKDPK 251
DB 263 ALLKFVDKDPK 273

RESULT 12

AAAR63923
ID AAR63923 standard; protein; 251 AA.
XX AAR63923;
XX 25-MAR-2003 (revised)
DT 27-JUL-1995 (first entry)
XX XX
XX Type I RIP gelonin analog Gel(C103).
XX Type I ribosome-inactivating proteins; RIPS; gelonin;
KW cytotoxic therapeutic agents; autoimmune disease; cancer;
KW graft-versus-host disease.
XX Gelonium multiflorum.
XX WO9426910-A1.
XX 24-NOV-1994.
XX 12-MAY-1994; 94WO-US005348.
XX 12-MAY-1993; 93US-00064691.
XX (XOMA) XOMA CORP.
XX Better MD, Carroll SF, Studnicka GW;
XX WPI; 1995-006804/01.
XX Polynucleotide(s) encoding type I ribosome-inactivating proteins - which
PT are suitable for use as components of cytotoxic therapeutic agents.
XX Example 3; Page 187-188; 221pp; English.
XX AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating
CC

CC protein (RIP) gelonin, one of the nine RIPs described in AAR63903-R63911.
CC RIPs are key components of cytotoxic therapeutic agents (CTAs), which
CC include gene fusion products and immunoconjugates. CTAs may be used to
CC selectively eliminate any cell type to which a RIP component is
CC targeted, by the specific binding capacity of the second component of
CC the agent. They can be used in the treatment of diseases where the
CC elimination of a particular cell type is desired, such as autoimmune
CC disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX
SQ Sequence 251 AA;

Query Match 99.0%; Score 1264; DB 2; Length 251;
Best Local Similarity 98.8%; Pred. No. 1e-118; Indels 0; Gaps 0;
Matches 248; Conservative 0; Mismatches 3;
QY 1 GLDVSFSTKGATITVYVNFNLRLVRLKPEGNHGIPLLRKADDPGKAFVLVALSNDN 60
DB 1 GLDVSFSTKGATITVYVNFNLRLVRLKPEGNHGIPLLRKADDPGKCFVLVALSNDN 60
QY 61 GOLAEIAIDVTSVYVVGQVNRNSYFFPKADPAAYEGLFKNTIKTRLHFGSGYPSLEGEK 120
DB 61 GOLAEIAIDVTSVYVVGQVNRNSYFFPKADPAAYEGLFKNTIKTRLHFGSGYPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETASSLLVVIQVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETASSLLVVIQVSEAAARFTFIENQIRNN 180
QY 181 FQQRIRPANNITISLENKWKGLSFQIRTSANGMFSEAVELEERANGKYYVTVAVDQVKPKI 240
DB 181 FQQRIRPANNITISLENKWKGLSFQIRTSANGMFSEAVELEERANGKYYVTVAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 13
AAR63921
ID AAR63921 standard; protein; 251 AA.
XX
AC AAR63921;
XX
DT 25-MAR-2003 (revised)
DT 27-JUL-1995 (first entry)
XX
DE Type I RIP gelonin analog Gel(C10).
XX
KW Type I ribosome-inactivating proteins; RIPs; gelonin;
KW cytotoxic therapeutic agents; autoimmune disease; cancer;
KW graft-versus-host disease.
XX
OS Gelonium multiflorum.
XX
PN W09426910-A1.
XX
PD 24-NOV-1994.
XX
PF 12-MAY-1994; 94WO-US005348.
XX
PR 12-MAY-1993; 93US-00064691.
XX
PA (XOMA) XOMA CORP.
XX
PI Better MD, Carroll SF, Studnicka GW;
XX
DR WPI; 1995-006804/01.
XX
PT Polynucleotide(s) encoding type I ribosome-inactivating proteins - which
PT are suitable for use as components of cytotoxic therapeutic agents.
XX
PS Example 3; Page 186; 221pp; English.

CC AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating
CC protein (RIP) gelonin, one of the nine RIPs described in AAR63903-R63911.
CC RIPs are key components of cytotoxic therapeutic agents (CTAs), which
CC include gene fusion products and immunoconjugates. CTAs may be used to
CC selectively eliminate any cell type to which a RIP component is
CC targeted, by the specific binding capacity of the second component of
CC the agent. They can be used in the treatment of diseases where the
CC elimination of a particular cell type is desired, such as autoimmune
CC disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX
SQ Sequence 251 AA;

Query Match 98.7%; Score 1261; DB 2; Length 251;
Best Local Similarity 98.8%; Pred. No. 2e-118; Indels 0; Gaps 0;
Matches 248; Conservative 0; Mismatches 3;
QY 1 GLDVSFSTKGATITVYVNFNLRLVRLKPEGNHGIPLLRKADDPGKAFVLVALSNDN 60
DB 1 GLDVSFSTKGATITVYVNFNLRLVRLKPEGNHGIPLLRKADDPGKCFVLVALSNDN 60
QY 61 GOLAEIAIDVTSVYVVGQVNRNSYFFPKADPAAYEGLFKNTIKTRLHFGSGYPSLEGEK 120
DB 61 GOLAEIAIDVTSVYVVGQVNRNSYFFPKADPAAYEGLFKNTIKTRLHFGSGYPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETASSLLVVIQVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETASSLLVVIQVSEAAARFTFIENQIRNN 180
QY 181 FQQRIRPANNITISLENKWKGLSFQIRTSANGMFSEAVELEERANGKYYVTVAVDQVKPKI 240
DB 181 FQQRIRPANNITISLENKWKGLSFQIRTSANGMFSEAVELEERANGKYYVTVAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 14
AAR63918
ID AAR63918 standard; protein; 251 AA.
XX
AC AAR63918;
XX
DT 25-MAR-2003 (revised)
DT 27-JUL-1995 (first entry)
XX
DE Type I RIP gelonin analog Gel(C248).
XX
KW Type I ribosome-inactivating proteins; RIPs; gelonin;
KW cytotoxic therapeutic agents; autoimmune disease; cancer;
KW graft-versus-host disease.
XX
OS Gelonium multiflorum.
XX
PN W09426910-A1.
XX
PD 24-NOV-1994.
XX
PF 12-MAY-1994; 94WO-US005348.
XX
PR 12-MAY-1993; 93US-00064691.
XX
PA (XOMA) XOMA CORP.
XX
PI Better MD, Carroll SF, Studnicka GW;
XX
DR WPI; 1995-006804/01.
XX
PT Polynucleotide(s) encoding type I ribosome-inactivating proteins - which
PT are suitable for use as components of cytotoxic therapeutic agents.
XX
PS Example 3; Page 183-184; 221pp; English.

XX AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating
 CC protein (RIP) gelonin, one of the nine RIPs described in AAR63903-R63911.
 CC RIPs are key components of cytotoxic therapeutic agents (CTAs), which
 CC include gene fusion products and immunoconjugates. CTAs may be used to
 CC selectively eliminate any cell type to which a RIP component is
 CC targeted, by the specific binding capacity of the second component of
 CC the agent. They can be used in the treatment of diseases where the
 CC elimination of a particular cell type is desired, such as autoimmune
 CC disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to
 CC correct PN field.)
 XX
 SQ Sequence 251 AA;

Query Match 98.7%; Score 1261; DB 2; Length 251;
 Best Local Similarity 98.8%; Pred. No. 2e-118;
 Matches 248; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 GLDTVSFSTKGATYITVYVNFLELRVCLKPEGNHGIPLLRKADDPGKAFVLVALSNDN 60
 Db 1 GLDTVSFSTKGATYITVYVNFLELRVCLKPEGNHGIPLLRKADDPGKCFVLVALSNDN 60
 Qy 61 GOLAEIAIDVTSVYVVGQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
 Db 61 GOLAEIAIDVTSVYVVGQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
 Qy 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQWVSEAAARPTFIENQIRNN 180
 Db 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQWVSEAAARPTFIENQIRNN 180
 Qy 181 FQQRIRPANNTISLENKWGKLSFOIRTSGANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
 Db 181 FQQRIRPANNTISLENKWGKLSFOIRTSGANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
 Qy 241 ALLKFVDCDPK 251
 Db 241 ALLKFVDCDPK 251

RESULT 15

AAR63920
 ID AAR63920 standard; protein; 251 AA.

XX AAR63920;

XX AC
 XX XX
 DT 25-MAR-2003 (revised)
 DT 27-JUL-1995 (first entry)

XX Type I RIP gelonin analog Gel (C244).

XX Type I ribosome-inactivating proteins; RIPs; gelonin;
 KW cytotoxic therapeutic agents; autoimmune disease; cancer;
 KW graft-versus-host disease.

XX Gelonium multiflorum.

XX WO9426910-A1.

XX 24-NOV-1994.

XX 12-MAY-1994; 94WO-US005348.

XX 12-MAY-1993; 93US-00064691.

XX (XOMA) XOMA CORP.

XX Better MD, Carroll SF, Studnicka GW;

XX WPI; 1995-006804/01.

XX Polynucleotide(s) encoding type I ribosome-inactivating proteins - which
 PT are suitable for use as components of cytotoxic therapeutic agents.

XX

PS Example 3; Page 185; 22lpp; English.

XX AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating
 CC protein (RIP) gelonin, one of the nine RIPs described in AAR63903-R63911.
 CC RIPs are key components of cytotoxic therapeutic agents (CTAs), which
 CC include gene fusion products and immunoconjugates. CTAs may be used to
 CC selectively eliminate any cell type to which a RIP component is
 CC targeted, by the specific binding capacity of the second component of
 CC the agent. They can be used in the treatment of diseases where the
 CC elimination of a particular cell type is desired, such as autoimmune
 CC disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to
 CC correct PN field.)
 XX

SQ Sequence 251 AA;

Query Match 98.7%; Score 1261; DB 2; Length 251;
 Best Local Similarity 98.8%; Pred. No. 2e-118;
 Matches 248; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 GLDTVSFSTKGATYITVYVNFLELRVCLKPEGNHGIPLLRKADDPGKAFVLVALSNDN 60
 Db 1 GLDTVSFSTKGATYITVYVNFLELRVCLKPEGNHGIPLLRKADDPGKCFVLVALSNDN 60
 Qy 61 GOLAEIAIDVTSVYVVGQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
 Db 61 GOLAEIAIDVTSVYVVGQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
 Qy 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQWVSEAAARPTFIENQIRNN 180
 Db 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQWVSEAAARPTFIENQIRNN 180
 Qy 181 FQQRIRPANNTISLENKWGKLSFOIRTSGANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
 Db 181 FQQRIRPANNTISLENKWGKLSFOIRTSGANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
 Qy 241 ALLKFVDCDPK 251
 Db 241 ALLKFVDCDPK 251

Search completed: February 10, 2006, 10:05:04
 Job time : 137.614 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.
OM protein - protein search, using sw model
Run on: February 10, 2006, 10:05:19 ; Search time 34.2694 Seconds
(without alignments)
704.723 Million cell updates/sec
Title: US-10-717-243-101
Perfect score: 1277
Sequence: 1 GLDTSVSTKGTATYTYNPF.....AVDQVKPKIALKFDKDPK 251
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : PIR 80:.*
1: piri:.*
2: piri2:.*
3: piri3:.*
4: piri4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1269	99.4	316	2	JT0753
2	353.5	27.7	245	2	JC4840
3	348	27.3	286	2	S25560
4	346	27.1	576	1	RLQSGD
5	343	26.9	286	2	JC4235
6	337.5	26.4	564	1	RLCSAG
7	334.5	26.2	527	2	S32430
8	332.5	26.0	294	2	S28421
9	330	25.8	251	2	C39761
10	327	25.6	313	2	S17757
11	323	25.3	289	1	RLT2T
12	321	25.1	528	1	TZLSA
13	317	24.8	247	2	JU0393
14	317	24.8	289	2	JC5606
15	313.5	24.5	261	2	JE0401
16	312	24.4	247	2	JC5032
17	310.5	24.3	277	2	S22494
18	304.5	23.8	254	2	PD0018
19	299	23.4	528	2	S32431
20	299	23.4	562	2	S16022
21	292	22.9	286	1	RLPUGG
22	290.5	22.7	570	2	S62627
23	287.5	22.5	278	2	JN0108
24	274	21.5	250	2	JN0108
25	215.5	16.9	278	2	A39817
26	210	16.4	272	2	JC4811
27	204	16.0	310	2	S46239
28	195	15.3	40	2	S17574
29	184.5	14.4	253	2	S28542

ALIGNMENTS

RESULT 1

JT0753

rRNA N-glycosidase (EC 3.2.2.22) precursor - Gelonium multiflorum

N:Alternate names: gelonin; type I ribosome-inactivating protein

C:Species: Gelonium multiflorum

C>Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 09-Jul-2004

C:Accession: JT0753; S16489

R:Nolan, P.A.; Garrison, D.A.; Better, M.

Gene 134, 223-227, 1993

A:Title: Cloning and expression of a gene encoding gelonin, a ribosome-inactivating protein

A:Reference number: JT0753; MUID:94085781; PMID:7916721

A:Accession: JT0753

A:Molecule type: mRNA

A:Residues: 1-316 <NOI>

R:Cross-references: UNIPROT:P33186; UNIPARC:UPI0000133948; GB:U12243; NID:G388633; PIDN

C:Rimotecucchi, P.C.; Lazzarini, A.M.; Barbieri, L.; Stirpe, F.; Sorio, M.; Lappi, D.

Int. J. Pept. Protein Res. 33, 263-267, 1989

A:Title: N-terminal sequence of some ribosome-inactivating proteins.

A:Reference number: S16331; MUID:89326691; PMID:2753596

A:Accession: S16489

A:Molecule type: protein

A:Residues: 47-89, 'K', 91-92, 'D' <MON>

A:Cross-references: UNIPARC:UPI0000177F26

C:Function:

A:Description: hydrolyzes the N-glycosidic bond of a specific adenosine in 28S rRNA the

C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology

C:Keywords: glycosidase; hydrolase

F:1-46/Domain: signal sequence #status predicted <SIG>

F:47-316/Product: ribosomal RNA N-glycosidase #status predicted <MAT>

F:53-294/Domain: rRNA N-glycosidase homology <RNG>

Query Match 99.4%; Score 1269; DB 2; Length 316;

Best Local Similarity 99.2%; Pred. No. 5.7e-97;

Matches 249; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY

1 GLDTSVSTKGTATYTYNPNELRVKLPKGNHGIPLLRKADDPGKAFVLVALSDN 60

47 GLDTSVSTKGTATYTYNPNELRVKLPKGNHGIPLLRKADDPGKAFVLVALSDN 106

QY

61 QQLAEIAIDVTSVYVVGQVRNRSYFFKADPAAYEGLFQNTIKTRLHFGSGSPSLEGEK 120

107 QQLAEIAIDVTSVYVVGQVRNRSYFFKADPAAYEGLFQNTIKTRLHFGSGSPSLEGEK 166

QY

121 AYRETTDGIPLRIGIKKLDENADNPKTEIASLLVVTQMSAARFTFIENQIRN 180

167 AYRETTDGIPLRIGIKKLDENADNPKTEIASLLVVTQMSAARFTFIENQIRN 226

QY

181 FQOIRPANNITISLENKWKLSFQIRTSANGMFSEAELEERANGKYYVTAVDQVKPKI 240

227 FQOIRPANNITISLENKWKLSFQIRTSANGMFSEAELEERANGKYYVTAVDQVKPKI 286

QY

241 ALLKFDVKDPK 251

Db 287 ALLKFVDKOPK 297
|||||
RESULT 2
JC4840
rRNA N-glycosidase (EC 3.2.2.22) trichoanguina - snake gourd
C;Species: Trichosanthes anguina (snake gourd)
C;Date: 15-Aug-1996 #sequence_revision 24-Oct-1997 #text_change 05-Dec-1997
C;Accession: JC4840; J070701; J0677
R;Chow, L.P.; Kamo, M.; Lin, J.Y.; Wang, S.H.; Ueno, Y.; Tsugita, A.
Biomed. Sci. 3, 178-186, 1996
A;Title: Amino acid of sequence of trichoanguina, a ribosomal-inactivating protein from
A;Reference number: JC4840
A;Accession: JC4840
A;Molecule type: protein
A;Residues: 1-132,'S',134-245 <CHO1>
A;Cross-references: UNIPARC:UPI0000177F1A
A;Experimental source: seed
A;Note: the sequence in Fig. 2 is inconsistent with the sequence data presented in Table
R;Chow, L.P.; Kamo, M.; Lin, J.Y.; Ueno, Y.; Tsugita, A.
submitted to JIPID, August 1995
A;Description: Amino acid sequence of trichoanguina, a ribosomal-inactivating protein fr
A;Reference number: J0677
A;Accession: J070701
A;Molecule type: protein
A;Residues: 1-50,'L',52-245 <CHO2>
A;Cross-references: UNIPARC:UPI0000177F1B
C;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
C;Keywords: glycoprotein; glycosidase; hydrolase; phosphoprotein; seed
F;4-242/Domain: rRNA N-glycosidase homology <RNG>
F;51,201/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;70,158,161/Active site: Tyr, Glu, Arg #status predicted
F;155/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
Query Match 27.7%; Score 353.5; DB 2; Length 245;
Best Local Similarity 36.3%; Pred. No. 9.5e-22;
Matches 91; Conservative 44; Mismatches 95; Indels 21; Gaps 7;
QY 5 VSFSTKGATITVYVNFLELRVKLKPEGNHSHGIPILLRKKADDPGKAPVLVALSNDNGOLA 64
Db 2 VSFDLSTATKKSYSFTQURDALPTQGVIGYIPLIPSTASG-SQRFPRFNLTYNDET 60
QY 65 EIAIDVTSVYVGVQVRNRSYFFKADPDAAYEGLFKNTIKTRLHPFGSYPSE--GEKA 121
Db 61 TVAVDVTVYVAVRADAVSYFFEDTPAEAFKLIFAGTKTVKLPYSGNDYKLSQSVVGKQ- 119
QY 122 YRETTDLGIEPLRIGIKKLDENAI--YKPTFIASSLLVVIQMVSEARPTFIENQIR 178
Db 120 -RDMIELGIPAL-----SSAITNNVYDYQSTAAALVLQSTAEARFYIEQQVS 170
QY 179 NNFQRIIPANNTISLENKWKLSFQIRTS--ANGMFSEAVELERANGKYYV--TAVD 234
Db 171 SHLSNFPNQAVISLENKWKLSKQIQIANRTGHGQFENPVELYNPDGTRFSVYTSAG 230
QY 235 QVRFKIALKRF 245
Db 231 VVRGNKILLY 241
RESULT 3
S25560
rRNA N-glycosidase (EC 3.2.2.22) momordin II - balsam apple
C;Species: Momordica balsamina (balsam apple)
C;Date: 25-Feb-1994 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C;Accession: S25560
R;Ortigao, M.; Better, M.
Nucleic Acids Res. 20, 4662, 1992
A;Title: Momordin II, a ribosome inactivating protein from Momordica balsamina, is homol
A;Reference number: S25560; MUID:93027170; PMID:1408771
A;Accession: S25560
A;Status: preliminary
A;Molecule type: mRNA

A;Residues: 1-286 <ORT>
A;Cross-references: UNIPROT:P29339; UNIPARC:UPI0000133937; EMBL:Z12175; NID:g19525; PID:
C;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
C;Keywords: glycosidase; hydrolase
F;27-264/Domain: rRNA N-glycosidase homology <RNG>
Query Match 27.3%; Score 348; DB 2; Length 286;
Best Local Similarity 37.4%; Pred. No. 3.3e-21;
Matches 91; Conservative 34; Mismatches 108; Indels 10; Gaps 5;
QY 5 VSFSTKGATITVYVNFLELRVKLKPEGNHSHGIPILLRKKADDPGKAPVLVALSNDNGOLA 64
Db 25 VNFDSLSTATKTYTFIEDFRATLFPESHKVDYDIPLYSTISD-SRRFILLDTSTAYEYI 83
QY 65 EIAIDVTSVYVGVQVRNRSYFFKADPDAAYEGLFKNTIKTRLHPFGSYPSE--GEKAYR 123
Db 84 SVAIDVTNVYVAVYTRDVSYFFKESPPPEAYNLPKGRKTLPTVTGNYENLQTAHKIR 143
QY 124 ETTDLGIEPLRIGIKKLDENAI--YKPTFIASSLLVVIQMVSEARPTFIENQIRNFFQ 183
Db 144 ENIDLGLPALSSAI-----TTLFYNAQSAPSAALLVLQTTAAEARFKYIERHVAKYVAT 198
QY 184 RIRPANNTISLENKWKLSFQI--RTSGANGMFSEAVELERANGKYYVTVAVDQ--VKPKI 240
Db 199 NFKPNLAIISLENQWSALSQKIFLAQNGGKFRNPVDLIKPTGERFQVTNVDSDVVKGI 258
QY 241 ALL 243
Db 259 KLL 261
RESULT 4
RLCSD
ricin D precursor - castor bean
N;Contains: rRNA N-glycosidase (EC 3.2.2.22)
C;Species: Ricinus communis (castor bean)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: A24041; S20513; A24614; A03372; A24010; A03374; S10903
R;Halling, K.C.; Halling, A.C.; Murray, E.E.; Ladin, B.F.; Houston, L.L.; Weaver, R.F.
Nucleic Acids Res. 13, 8019-8033, 1985
A;Title: Genomic cloning and characterization of a ricin gene from Ricinus communis.
A;Reference number: A24041; MUID:86067214; PMID:2999712
A;Accession: A24041
A;Molecule type: DNA
A;Residues: 1-576 <HAL>
A;Cross-references: UNIPROT:P02879; UNIPARC:UPI00001338E8; GB:X03179; NID:g21082; PIDN:
R;Tregear, J.W.; Roberts, L.M.
Plant Mol. Biol. 18, 515-525, 1992
A;Title: The lectin gene family of Ricinus communis: cloning of a functional ricin gene
A;Reference number: S20513; MUID:92163016; PMID:1371405
A;Accession: S20513
A;Molecule type: DNA
A;Residues: 1-576 <TRE>
A;Cross-references: UNIPARC:UPI00001338E8; EMBL:X52908; NID:g21084; PIDN:CAA37095.1; PID:
R;Lamb, F.I.; Roberts, L.M.; Lord, J.M.
Eur. J. Biochem. 148, 265-270, 1985
A;Title: Nucleotide sequence of cloned cDNA coding for preproricin.
A;Reference number: A24614; MUID:85179479; PMID:3838723
A;Accession: A24614
A;Molecule type: mRNA
A;Residues: 12-75,'D',77-550,'R',552-576 <LAM>
A;Cross-references: UNIPARC:UPI000011D47E; GB:X02388; NID:g21077; PIDN:CAA26230.1; PID:
R;Yoshitake, S.; Funatsu, G.; Funatsu, M.
Agric. Biol. Chem. 42, 1267-1274, 1978
A;Title: Isolation and sequences of peptic peptides, and the complete sequence of ile c
A;Reference number: A03372
A;Accession: A03372
A;Molecule type: protein
A;Residues: 36-97,'Q',99-109,'S',111-269,'D',272-283,'L',285-288,290-302 <YOS>
A;Cross-references: UNIPARC:UPI0000174677
A;Note: this paper cites the others in the series providing experimental details for th
R;Araki, T.; Funatsu, G.
PEBS Lett. 191, 121-124, 1985

•

J. Biol. Chem. 260, 15682-15686, 1985
A;Title: The primary sequence of Ricinus communis agglutinin. Comparison with ricin.
A;Reference number: A24261; MUID:86059449; PMID:2999130
A;Accession: A24261
A;Molecule type: mRNA
A;Residues: 1-564 <ROB>
A;Cross-references: UNIPROT:P06750; UNIPARC:UPI00001256B9; GB:M12089; NID:g169700; PIDN:
R;Araki, T.; Yoshioka, Y.; Funatsu, G.
Biochim. Biophys. Acta 872, 277-285, 1986
A;Title: The complete amino acid sequence of the B-chain of the Ricinus communis aggluti
A;Reference number: A24210
A;Accession: A24210
A;Molecule type: protein
A;Residues: 303-325, F, 327-330, T', 332-361, 'D', 363-373, 'G', 375-403, 'T', 405-551, 'V', 553-
A;Cross-references: UNIPARC:UPI0000174679
C;Comment: This protein has strong agglutinating activity and weak cytotoxicity compared
C;Superfamily: ricin; rRNA N-glycosidase homology
C;Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; RNA binding; seed
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-290/Product: agglutinin chain A #status predicted <ACH>
F;35-281/Domain: rRNA N-glycosidase homology <RNG>
F;303-564/Product: agglutinin chain B #status experimental <BCH>
F;319-361,362-402,405-443,450-485,489-528,531-564/Region: 40-residue repeats
F;34,259/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;104,147,231,232/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F;200,203/Active site: Glu, Arg #status predicted
F;282-306,322-341,365-382,453-466,492-509/Disulfide bonds: #status predicted
F;324,337,348/Binding site: N-acetylgalactosamine (Asp, Glu, Asn) #status predicted
F;397,437/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;536,557/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted
Query Match 26.4%; Score 337.5; DB 1; Length 564;
Best Local Similarity 36.3%; Pred. No. 6.1e-20;
Matches 91; Conservative 42; Mismatches 105; Indels 13; Gaps 7;
QY 5 VPSSTKGATITVYVNFLELRLVKLPKPGN-SHGIPILRKKADDP-GKAFVLVSLNDNGQ 62
DB 33 INFTTADATVESYTNFIRAVRSHLTTCGADVRRHIEPVLPRVGLPIQRFILVELSHL 92
QY 63 LABIAIDVTSVYVGVQVNRYSFFKADP-----AAYELFKNTIKT-RLHFGGYSPL 116
DB 93 SVTLALDVINAVVGCAGNSAFPH--PDNQDAEAITHLFDVQNSFTFAFGNYDRL 150
QY 117 EGEKAVRETTDLGIEPLIRIGIKKLDENADINYPKPTIASLLVVIQMVSEARFTPIENQ 176
DB 151 EQLGGLRENIELGTGLEDAISALYYSTGQTPTLARSFMVCIQMISEARFQYIEGE 210
QY 177 IRN-NFOQIRPANNTISLENKWKLSQIRTSANGWFSEAVELERANGKYYVYVD 234
DB 211 MTRIRYRRSAPDPSPVITLNSWGRSLTAIQESN-QGAPASPIQLQRNGSKFNVDVS 269
QY 235 QVKPKIALLKPF 245
DB 270 ILIPITALVY 280
RESULT 7
abrin-b precursor - Indian licorice (fragment)
N;Contains: rRNA N-glycosidase (EC 3.2.2.22)
C;Species: Abrus precatorius (Indian licorice)
C;Date: 30-Sep-1993 #sequence_revision 01-Aug-1997 #text_change 09-Jul-2004
C;Accession: S32430; JCI399
R;Hung, C.H.; Lee, M.C.; Lee, T.C.; Lin, J.Y.
J. Mol. Biol. 229, 263-267, 1993
A;Title: Primary structure of three distinct isoabrin determined by cDNA sequencing. Co
A;Reference number: S32429; MUID:93132798; PMID:8421313
A;Accession: S32430
A;Molecule type: mRNA
A;Residues: 1-527 <HUN>
A;Cross-references: UNIPROT:Q06077; UNIPARC:UPI0000125160; GB:M98345; NID:g166296; PIDN:
R;Kimura, M.; Sumizawa, T.; Funatsu, G.
Biosci. Biotechnol. Biochem. 57, 166-169, 1993

A;Title: The complete amino acid sequences of the B-chains of Abrin-a and Abrin-b, toxic
A;Reference number: JCI398; MUID:93169023; PMID:7763422
A;Accession: JCI399
A;Molecule type: protein
A;Residues: 260-281, 'D', 283-290, 'N', 292-349, 'PQ', 352-377, 'N', 379-425, 'M', 427, 'D', 429-430
A;Cross-references: UNIPARC:UPI00001772PA
A;Experimental source: seed
C;Superfamily: ricin; rRNA N-glycosidase homology
C;Keywords: disulfide bond; duplication; glycoprotein; glycosidase; hydrolase; lectin; r
F;1-250/Product: abrin-b chain A #status predicted <ACH>
F;7-245/Domain: rRNA N-glycosidase homology <RNG>
F;260-527/Product: abrin-b chain B #status experimental <BCH>
F;282-324,325-365,368-406,413-448,452-491,494-527/Region: 40-residue repeats
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
F;74,113,194,195/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F;110,360,400/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;163,166/Active site: Glu, Arg #status predicted
F;246-268,285-304,328-345,416-429,455-472/Disulfide bonds: #status predicted
F;287,311/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted
F;499,520/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted
Query Match 26.2%; Score 334.5; DB 2; Length 527;
Best Local Similarity 37.7%; Pred. No. 9.9e-20;
Matches 97; Conservative 34; Mismatches 103; Indels 23; Gaps 9;
QY 5 VPSSTKGATITVYVNFLELRLVKLPKPGN-SHGIPILRKKADDP-----GKAFVLVSLND 59
DB 5 IKFTTTEGATSQSYKQFIEALRQL-TGGLIHGIPVL-----PDPTLQERNRYISVELSNS 59
QY 60 NQLAEIAIDVTSVYVGVQVNRYSFFKADPAAYEGLFKNTIKTRLHFGGYSPLSG- 118
DB 60 DTESIETAGIDVSNVAVVAYRAGNRSYFURDAPTSASRYLFTGQYSLRFGNSYIDLRL 119
QY 119 EKAVRETTDLGIEPLIRIGIKKLDENADINYPKPTIASLLVVIQMVSEARFTPIENQ-- 176
DB 120 ARQTRQQLPLGLQALRHAIPLSQGTDDQ-----EIARTLIVIOASEAARYRFTSYRVG 175
QY 177 --IRNFQOIRPANNTISLENKWKLSQIRTSANGWFSEAVELERANGKYYVYVAV- 233
DB 176 VSIRTN--TAFQPDAMISLENNDNLGGVQQS-VQDTPFNAVTILRSVNNQFVDSLT 232
QY 234 DVKPKIALLKPFVDKDP 250
DB 233 HOSVAVLALMLFVCNPP 249
RESULT 8
S28421
rRNA N-glycosidase (EC 3.2.2.22) PAP-alpha - Virginian pokeweed
N;Alternate names: antiviral protein alpha-PAP
C;Species: Phytolacca americana (Virginian pokeweed)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: S28421
R;Kataoka, J.; Habuka, N.; Masuta, C.; Miyano, M.; Koiwai, A.
Plant Mol. Biol. 20, 879-886, 1992
A;Title: Isolation and analysis of a genomic clone encoding a pokeweed antiviral protei
A;Reference number: S28421; MUID:93099240; PMID:1281438
A;Accession: S28421
A;Molecule type: DNA
A;Residues: 1-294 <KAT>
A;Cross-references: UNIPROT:Q03464; UNIPARC:UPI0000133946; EMBL:D10600; NID:g218010; PFI
C;Superfamily: rRNA N-glycosidase homology
C;Keywords: glycosidase; hydrolase
F;30-278/Domain: rRNA N-glycosidase homology <RNG>
Query Match 26.0%; Score 332.5; DB 2; Length 294;
Best Local Similarity 32.2%; Pred. No. 6.5e-20;
Matches 85; Conservative 50; Mismatches 102; Indels 27; Gaps 8;
QY 2 LDTVSFSTKGATITVYVNFLELRLVKLK-PEGNSHGIPILRKKADDPGKAFVLVSLNDN 60
DB 25 INTITFDVGNATINKYATPMKSIHQAKDPTLKCYGIPMLPNTNLTP--KYLAVTLQDSS 82

RESULT 13
JU0393
Karasurin
C:Species
C>Date: 3
C:Accessi
R:Toyokaw
Chem. Phat
A>Title:
A:Referenc
A:Accessib
A:Molecul
A:Residue
A:Cross-r
A>Note: s
C:Superfa
C:Keyworc
F:4-243/D
Query M Best LC Matches
QY
Dd
QY
Dd
QY
Dd
QY
Dd
QY
Dd
QY
Dd
RESULT 14
JCS606
Karasurin
N:Contain
C:Specie
C>Date: 2
C:Accessi
R:Mizukam
Biol. Phat
A>Title:
A:Referenc
A:Accessib
A:Molecul
A:Residue
A:Cross-r
R:Kondo,
Biol. Phat
A>Title:
A:Referenc
A:Accessi
A>Status
A:Molecul
A:Residue
A:Cross-r
C:Comment
C:Comment
C:Superfa

RESULT 14
JC5606
karasurin
N:Contain
C:Species
C:date: 2
R:Access
R:Mizukam
Blol. Phal
A:Title:
A:Referen
A:Access
A:Molecu
A:Residu
A:Cross-
R:Kondo
Blol. Phal
A:Title:
A:Referen
A:Access
A:Status
A:Molecu
A:Residu
A:Cross-
C:Comment
C:Superfig

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 10, 2006, 10:00:34 ; Search time 212.1 Seconds
(without alignments)
834.927 Million cell updates/sec

Title: US-10-717-243-101
Perfect score: 1277
Sequence: 1 GLDVTSTSTGKATITYVNF.....AVDQVQPKIALLKFDKDPK 251

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1269	99.4	316	1	RIPG_GELMU
2	1235.5	96.8	258	1	Q99E44 gelonium mu
3	398.5	31.2	581	2	Q94BW5 CINCA
4	397.5	31.1	580	2	Q94BW3 CINCA
5	396.5	31.0	549	2	Q9FV22 CINCA
6	391	30.6	299	2	Q8GZ99 9ROSI
7	390.5	30.6	580	2	Q94BW4 CINCA
8	365.5	28.6	563	2	Q8GT32 SAMNI
9	359.5	28.2	297	2	Q8GZP0 9ROSI
10	356	27.9	563	1	NIGB SAMNI
11	356	27.9	563	2	Q945S2 SAMNI
12	352.5	27.6	563	2	Q04367 SAMNI
13	348	27.3	264	2	Q684J5 MOMCH
14	348	27.3	286	1	RIP2 MOMBA
15	348	27.3	286	1	RIP3 MOMCH
16	348	27.3	286	2	Q5PZ05 MOMCH
17	347	27.2	541	2	Q41174 RICCO
18	346	27.1	576	1	RIC1 RICCO
19	343.5	26.9	265	1	RIP2 PHYDI
20	341.5	26.7	294	1	RIP1 TRIAN
21	341.5	26.7	564	2	Q9AVR2 9DIPS
22	337.5	26.4	564	1	AGEL RICCO
23	337	26.4	282	1	RIP2_BRYDI
24	334.5	26.2	527	1	ABRP ABRPR
25	332.5	26.0	294	1	RIPA PHYAM
26	330.5	25.9	293	2	Q8VYU0 9ROSI
27	330.5	25.8	252	2	Q38760 ABRPR
28	329.5	25.8	294	2	Q8H1W1 PHYAM
29	328.5	25.7	275	2	Q84LJ1 GYNPE
30	327.5	25.6	277	2	Q84JRI GYNPE
31	327	25.6	313	1	RIP1 PHYAM

32	327	25.6	313	2	Q6PWU4 PHYAM
33	327	25.6	313	2	Q53YN2 PHYAM
34	326.5	25.6	277	2	Q8GV09 GYNPE
35	326	25.5	289	2	Q41216 TRIKI
36	325.5	25.5	275	2	Q8H1Y4 GYNPE
37	325.5	25.5	293	2	Q8S452 9ROSI
38	325.5	25.5	298	2	Q5F013 GYNPE
39	325	25.5	567	2	Q6H267 VISAL
40	323.5	25.3	277	2	Q8GV11 GYNPE
41	323	25.3	289	1	RIP1 TRIKI
42	323	25.3	289	2	Q94KE4 TRIKI
43	322	25.2	289	2	Q84SV8 TRIKI
44	321.5	25.2	565	2	Q04071 SAMNI
45	321	25.1	251	2	Q7DM12 ABRPR

ALIGNMENTS

RESULT 1					
ID	RIPG_GELMU	STANDARD;	PRT;	316 AA.	
AC	P33186;				
DT	01-OCT-1993 (Rel. 27, Created)				
DT	01-NOV-1995 (Rel. 32, Last sequence update)				
DT	10-MAY-2005 (Rel. 47, Last annotation update)				
DB	Ribosome-inactivating protein gelonin precursor (EC 3.2.2.22) (rRNA N-glycosidase).				
DB	Glycosidase.				
GN	Name=GEL;				
OS	Gelonium multiflorum (Euphorbiaceae himalayana).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;				
OC	rosids; eurosids I; Malpighiales; Euphorbiaceae; Crotonoideae;				
OC	Geloniaceae; Gelonium.				
OX	NCBI_TaxID=3379;				
OX	[1]				
RP	NUCLEOTIDE SEQUENCE.				
RX	MEDLINE=94085781; PubMed=7916721; DOI=10.1016/0378-1119(93)90097-M;				
RA	Nolan P.A., Garrison D.A., Better M.;				
RT	"Cloning and expression of a gene encoding gelonin, a ribosome-inactivating protein from Gelonium multiflorum.";				
RL	Gene 134:223-227(1993).				
RL	[2]				
RP	PROTEIN SEQUENCE OF 47-93.				
RP	TISSUE=Seed;				
RC	MEDLINE=89326691; PubMed=2753596;				
RX	Montecucchi P.-C., Lazzarini A.M., Barbieri L., Stirpe P., Soria M.,				
RA	Lappi D.;				
RT	"N-terminal sequence of some ribosome-inactivating proteins.";				
RL	Int. J. Pept. Protein Res. 33:263-267(1989).				
RL	[3]				
RP	X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).				
RX	MEDLINE=95333189; PubMed=7608981;				
RA	Hosur M.V., Nair B., Sathyanarthy P., Misquith S., Suroolia A.,				
RA	Kannan K.K.;				
RT	"X-ray structure of gelonin at 1.8-A resolution.";				
RL	J. Mol. Biol. 250:368-380(1995).				
CC	- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.				
CC	- SUBUNIT: Homodimer.				
CC	- SIMILARITY: Belongs to the ribosome-inactivating protein family.				
CC	Type 1 RIP subfamily.				
CC	-----				
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.				
CC	-----				
CC	EMBL; L12243; AAA16312.1; -; mRNA.				
DR	PIR; J07053; J07053.				
DR	HSSP; P09989; ILMRJ.				
DR	InterPro; IPR001574; RIP.				

DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 KW Direct protein sequencing; Glycoprotein; Hydrolase; Plant defense;
 KW Protein synthesis inhibitor; Signal; Toxin.
 FT SIGNAL 1 26 Potential.
 FT PROPEP 27 46
 FT CHAIN 47 297 Ribosome-inactivating protein gelonin.
 FT PROPEP 298 316 Removed in mature form.
 FT ACT_SITE 212 232
 FT CARBOHYD 235 235 N-linked (GlcNAc...).
 FT DISULFID 90 96
 FT CONFLICT 90 90 C -> K (in Ref. 2).
 FT CONFLICT 93 93 P -> D (in Ref. 2).
 SQ SEQUENCE 316 AA; 35419 MW; 1252F3E710901B85 CRC64;

Query Match 99.4%; Score 1269; DB 1; Length 316;
 Best Local Similarity 99.2%; Pred. No. 1.9e-97;
 Matches 249; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GLDTSVSTKGATYYTYVNFNLRLVKLPKPGNSHGIPLLRKADDPGKAFVLVALSNDN 60
 |||||
 Db 47 GLDTSVSTKGATYYTYVNFNLRLVKLPKPGNSHGIPLLRKADDPGKCFVLVALSNDN 106
 |||||

QY 61 GLAIAIDVTSVYVGVQVRNRSYFFKDAAPDAAYEGLFKNTIKRLHFGGSPSLEGEK 120
 |||||
 Db 107 GLAIAIDVTSVYVGVQVRNRSYFFKDAAPDAAYEGLFKNTIKRLHFGGSPSLEGEK 166
 |||||

QY 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTETIASLLVVIOMVSEAAARFTFENQIRNN 180
 |||||
 Db 167 AYRETTDLGIEPLRIGIKKLDENADNYKPTETIASLLVVIOMVSEAAARFTFENQIRNN 226
 |||||

QY 181 FQOIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
 |||||
 Db 227 FQOIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 286
 |||||

QY 241 ALLKFDVKDPK 251
 |||||
 Db 287 ALLKFDVKDPK 297
 |||||

RESULT 2
 Q939E4_GELMU PRELIMINARY; PRT; 258 AA.
 ID Q939E4; GELMU
 AC Q939E4;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE rRNA-glycosidase (EC 3.2.2.22) (rRNA N-glycosidase).
 OS Gelonium multiflorum (Euphorbiaceae Himalaya).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC rosids; eurosids I; Malpighiales; Euphorbiaceae; Crotonoideae;
 OC Geloniae; Gelonium.
 OX NCBI_TaxID=3979;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=96006751; PubMed=7553224;
 RA Rosenblum M.G., Kohr W.A., Beattie K.L., Beattie W.G., Marks W.,
 RA Toman P.D., Cheung L.;
 FT "Amino acid sequence analysis, gene construction, cloning, and
 RT expression of gelonin, a toxin derived from Gelonium multiflorum.";
 RL J. Interferon Cytokine Res. 15:547-555(1995).
 DR HSSP; P09989; 1MRJ.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR GO; GO:0030598; P:rRNA N-glycosylase activity; IEA.
 DR GO; GO:0005952; P:defense response; IEA.
 DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.

KW Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.
 SQ SEQUENCE 258 AA; 28826 MW; 13D68E673F4D6B06 CRC64;

Query Match 96.8%; Score 1235.5; DB 2; Length 258;
 Best Local Similarity 95.4%; Pred. No. 9.3e-95;
 Matches 247; Conservative 1; Mismatches 2; Indels 9; Gaps 2;

QY 1 GLDTSVSTKGATYYTYVNFNLRLVKLPKPGNSHGIPLLRKADDPGKAFVLVALSNDN 60
 |||||
 Db 1 GLDTSVSTKGATYYTYVNFNLRLVKLPKPGNSHGIPLLR-KGDDPGKCFVLVALSNDN 59
 |||||

QY 61 GLAIAIDVTSVYVGVQVRNRSYFFKDAAPDAAYEGLFKNTI-----KTRLHFGGS 112
 |||||
 Db 60 GLAIAIDVTSVYVGVQVRNRSYFFKDAAPDAAYEGLFKNTLFLFGKTRLHFGGS 119
 |||||

QY 113 YPSLEGEKAYRETTDLGIEPLRIGIKKLDENADNYKPTETIASLLVVIOMVSEAAARFTF 172
 |||||
 Db 120 YPSLEGEKAYRETTDLGIEPLRIGIKKLDENADNYKPTETIASLLVVIOMVSEAAARFTF 179
 |||||

QY 173 IENQIRNNFQOIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTV 232
 |||||
 Db 180 IENQIRNNFQOIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTV 239
 |||||

QY 233 VDQVKPKIALKFDVKDPK 251
 |||||
 Db 240 VDQVKPKIALKFDVKDPK 258
 |||||

RESULT 3
 Q94BW5_CINCA PRELIMINARY; PRT; 581 AA.
 ID Q94BW5; CINCA
 AC Q94BW5;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Type 2 ribosome-inactivating protein cinnamomin I precursor.
 OS Cinnamomum camphora (Camphor tree).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; magnoliids; Laurales; Lauraceae;
 OC Cinnamomum.
 OX NCBI_TaxID=13429;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=21889636; PubMed=11891062; DOI=10.1016/S0378-1119(01)00890-3;
 RA Yang Q., Liu R.S., Gong Z.Z., Liu W.Y.;
 RT "Studies of three genes encoding Cinnamomin (a type II RIP) isolated
 RL from the seeds of camphor tree and their expression patterns.";
 RL Gene 284:215-223(2002)
 DR EMBL; AY039801; AAK82458.1; -; Genomic_DNA.
 DR HSSP; P02879; 2AAI.
 DR GO; GO:0030598; P:rRNA N-glycosylase activity; IEA.
 DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
 DR InterPro; IPR000772; Ricin_B_lectin.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00652; Ricin_B_lectin; 2.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR SMART; SMO0458; RICIN; 2.
 DR PROSITE; PS50231; RICIN_B_LECTIN; 2.
 KW SIGNAL.
 FT SIGNAL 1 32 Potential.
 FT CHAIN 33 581 type 2 ribosome-inactivating protein cinnamomin I.
 SQ SEQUENCE 581 AA; 64215 MW; 6E8F5F8FBA3D196 CRC64;

Query Match 31.2%; Score 398.5; DB 2; Length 581;
 Best Local Similarity 39.7%; Pred. No. 1.8e-24;
 Matches 100; Conservative 46; Mismatches 99; Indels 13; Gaps 8;

QY 4 TVSFSTKGATYYTYVNFNLRLVKLPKPGNSHGIPLLRKADDPGKAFVLVALSNDN 59
 |||||
 Db 35 TVTFTTKNATKTSYTFQIFALRAQLASGEHPGIVMVERSTVPDSKRFILVELSNWAAD 94
 |||||


```

QY 60 NQGLAEIAIDVTSVTVGVQVNRNSYFFK-DAPDAAYEGLPKNTIKTRLHFGSGSPSLE 118
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
95 SP--VTLAVDVTVNAVYRTGSGFFLRDNPDPAIENLLPDKRYTFPFSGSYTDLEG 152
QY 119 EKA-YRETTDLGIEPLRIGIKKLDENAIIDNYKPTIASSLLVVIQWSEAAARFTFENQI 177
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
153 VAGERREILLGMDPLENAISALWISNLNQQR--ALARSLIVVIQWVAEAVRFRFIEYRV 210
QY 178 RNNFQ--QRIIPANNITISLENKWKLSFQIRTSANGMFSEAVELERANGKKYVTVAV-D 234
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
211 RGSISRAEMFRDPAMLSLENKWSALSNAVQSQNGGVFSSPVELRSISNKPYYVGSVD 270
QY 235 QVKPKIALLKVF 246
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
271 RVISGLAIMLFI 282

RESULT 4
Q94BW3_CINCA
ID Q94BW3_CINCA PRELIMINARY; PRT; 580 AA.
AC Q94BW3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Type 2 ribosome-inactivating protein cinnamomin III precursor.
OS Cinnamomum camphora (Camphor tree).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; magnoliids; Laurales; Lauraceae;
OC Cinnamomum.
OX NCBI_TaxID=13429;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=2188636; PubMed=11891062; DOI=10.1016/S0378-1119(01)00890-3;
RA Yang Q., Liu R.S., Gong Z.Z., Liu W.Y.;
RT "Studies of three genes encoding Cinnamomin (a type II Rip) isolated
RL from the seeds of camphor tree and their expression patterns.;"
RL Gene 284:215-223(2002).
DR HSSP; P02879; 2AAL.
DR GO; GO:0030598; P:negative regulation of protein biosynthesis; IEA.
DR EMBL; AY039803; AAK82460.1; -; Genomic_DNA.
DR GO; GO:0007148; P:negative regulation of protein biosynthesis; IEA.
DR InterPro; IPR000772; Ricin_B_lectin.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00652; Ricin_B_lectin; 2.
DR PRINTS; PR00396; SHIGARICIN.
DR SMART; SM00458; RICIN; 2.
DR PROSITE; PS50231; RICIN_B_LECTIN; 2.
KW Signal.
FT SIGNAL 1 32 Potential.
FT CHAIN 33 580 type 2 ribosome-inactivating protein
FT CINNAMOIN III.
SQ SEQUENCE 580 AA; 64421 MW; 940D10F01E7FB558 CRC64;

Query Match 31.1%; Score 397.5; DB 2; Length 580;
Best Local Similarity 39.8%; Pred. No. 2.1e-24;
Matches 101; Conservative 47; Mismatches 89; Indels 17; Gaps 9;

QY 4 TVSFSTKGATYTYVNFNLRLVKLPKGNHSHGIPLLRKKADDP-GKAFVLVALSN---D 59
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
35 TVTFTTKNATKTSYQTFEALRAQLASGEEPHGIPVVRERSTVPDSKRFILVELSNAAD 94
QY 60 NQGLAEIAIDVTSVTVGVQVNRNSYFFK-DAPDAAYEGLPKNTIKTRLHFGSGSPSLE- 117
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
95 SP--VTLAVDVTVNAVYRTGSGFFLRDNPDPAIENLLPDKRYTFPFSGSYTDLER 152
QY 118 --GEKAYRETTDLGIEPLRIGIKKLDENAIIDNYKPTIASSLLVVIQWSEAAARFTFEN 175
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
153 VAGER--REEILLGMDPLENAISALWISNLNQQR--ALARSLIVVIQWVAEAVRFRFIEY 208
QY 176 QIRNFP--QRIIPANNITISLENKWKLSFQIRTSANGMFSEAVELERANGKKYVTVAV 233
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
209 RVRESITRAEMFRDPAMLSLENKWSALSNAVQSQNGGVFSSPVELRSISNKPYYVGSV 268

```

```

QY 234 -DOVKPKIALLKVF 246
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
269 SDRVISGLAIMLFI 282

RESULT 5
Q9FV22_CINCA
ID Q9FV22_CINCA PRELIMINARY; PRT; 549 AA.
AC Q9FV22;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Type II ribosome-inactivating protein cinnamomin (fragment).
OS Cinnamomum camphora (Camphor tree).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; magnoliids; Laurales; Lauraceae;
OC Cinnamomum.
OX NCBI_TaxID=13429;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Xie L., Liu W.-Y., Wang E.-D.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF259548; AAF68978.2; -; mRNA.
DR HSSP; P02879; 2AAL.
DR GO; GO:0030598; P:rRNA N-glycosylase activity; IEA.
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR InterPro; IPR000772; Ricin_B_lectin.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00652; Ricin_B_lectin; 2.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR SMART; SM00458; RICIN; 2.
DR PROSITE; PS50231; RICIN_B_LECTIN; 2.
FT NON_TER 1
SQ SEQUENCE 549 AA; 60648 MW; 02607FE607CA44B0 CRC64;

Query Match 31.0%; Score 396.5; DB 2; Length 549;
Best Local Similarity 39.7%; Pred. No. 2.4e-24;
Matches 100; Conservative 46; Mismatches 93; Indels 13; Gaps 8;

QY 4 TVSFSTKGATYTYVNFNLRLVKLPKGNHSHGIPLLRKKADDP-GKAFVLVALSN---D 59
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
3 TVTFTTKNATKTSYQTFEALRAQLASGEEPHGIPVVRERSTVPDSKRFILVELSNAAD 62
QY 60 NQGLAEIAIDVTSVTVGVQVNRNSYFFK-DAPDAAYEGLPKNTIKTRLHFGSGSPSLE 118
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
63 SP--VTLAVDVTVNAVYRTGSGFFLRDNPDPAIENLLPDKRYTFPFSGSYTDLEG 120
QY 119 EKA-YRETTDLGIEPLRIGIKKLDENAIIDNYKPTIASSLLVVIQWSEAAARFTFENQI 177
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
121 VAGERREILLGMDPLENAISALWISNLNQQR--ALARSLIVVIQWVAEAVRFRFIEYRV 178
QY 178 RNNFQ--QRIIPANNITISLENKWKLSFQIRTSANGMFSEAVELERANGKKYVTVAV-D 234
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
179 RGSISRAEMFRDPAMLSLENKWSALSNAVQSQNGGVFSSPVELRSISNKPYYVGSVD 238
QY 235 QVKPKIALLKVF 246
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
239 RVISGLAIMLFI 250

RESULT 6
Q8GZN9_GROSI
ID Q8GZN9_GROSI PRELIMINARY; PRT; 239 AA.
AC Q8GZN9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Ribosome inactivating protein Euserratin 2 precursor
DE (EC 3.2.2.22).
GN Name=Rus2;
OS Euphorbia serrata.

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids I; Malpighiales; Euphorbiaceae; Euphorbiaoideae;
OC Euphorbleae; Euphorbia.
NCBI_TaxID=196589;
QN [1]_TaxID=
RN NUCLEOTIDE SEQUENCE.
RA Girbes T., Arias F.J., Benvenuto E.;
RT "Purification, characterization and molecular cloning of euserratin,
RT new type 1 ribosome-inactivating proteins from *Euphorbia serrata* L.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: A2457875; AAC15531.1; -, mRNA.
DR HSP; Q9AVR2; lHWN.
DR GO: GO:0016798; P:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO: GO:0030598; P:rRNA N-glycosylase activity; IEA.
DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
DR GO: GO:0006952; P:defence response; IEA.
DR GO: GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR GO: GO:0009405; P:pathogenesis; IEA.
DR InterPro: IPR001574; RIP.
DR Pfam: PF00161; RIP; 1.
DR PRINTS: PR00396; SHIGARICIN.
DR PROSITE: PS00275; SHIGA_RICIN; 1.
KW Glycosidase; Hydrolase; Plant defense; Protein synthesis inhibitor;
KW Signal; Toxin.
FT SIGNAL
FT CHAIN 1 23 Potential.
FT CHAIN 24 299 ribosome inactivating protein Euserratin
FT FT
FT FT
SQ SEQUENCE 299 AA; 33115 MW; DE791872B9CE2A7D CRC64;

Query Match 30.6%; Score 391; DB 2; Length 299;
Best Local Similarity 41.3%; Pred. No. 3.2e-24;
Matches 102; Conservative 36; Mismatches 97; Indels 12; Gaps 5

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Db :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
30 SVKFTHLASVGVSQSPFMSLRKLSDSGESHDIPLLRKPTEITNNKKTLNVLNLYDSQ 89
QY 63 LA-EIAVDTSVVYGVGRNRSYFFKDAPDAAYEGLFKNTIKTRLLHFPGSVPSLEGKA 121
Db |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
90 LSITAVTVNVYVYGYSAGNSFLLKDPASDKTLLFGQTNKITL---SSVDSVNNG 146
QY 122 YRETTDLGIEPIRLIGI---KKLDENADNYKPTETIASLLAVVIQMVEAAERTFIENQIR 178
Db |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
147 DRSKVGLGIGLSRSIDTLNFKNVGSVNVN----PKESILLVLIQWAEAAERFKIQLKIE 202
QY 179 NNFOQRIPANNITSLENKGKLSFQIRTSGANGMPSEAVEBRANKKYVTVAOVQVP 238
Db :|:|:|:|:~::~::|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
203>NNLLDEYKPDNDTI SYENNWEKLSSEQIQLSGTDGKPKKPVLTLLYANGTDKIYSTVAQVKP 262
QY 239 KIALLKF 245
Db |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
Db 263 DISILLY 269

RESULT 7
Q94BW4_CINCA PRELIMINARY; PRT; 580 AA.

ID Q94BW4_CINCA PRELIMINARY; AC Q94BW4;
AC Q94BW4; DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Type 2 ribosome-inactivating protein cinnamin II precursor.
OS Cinnamomum camphora (Camphor tree).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; magnoliids; Laurales; Lauraceae;
OC Cinnamomum.
NCBI_TaxID=13429;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=21988636; PubMed=11891062; DOI=10.1016/S0378-1119(01)00890-3;
RX Yang Q., Liu R.S., Gong Z.Z., Liu W.Y.;
RT "Studies of three genes encoding Cinnaminin (a type II RIP)-isolated

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 10, 2006, 10:37:59 ; Search time 163.937 Seconds
(without alignments)
639.727 Million cell updates/sec

Title: US-10-717-243-101

Perfect score: 1277

Sequence: 1 GLDTRVSTKGTATVTVNF.....AVDQVKPKIALLKFDVKDPK 251

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA_Main.*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1277	100.0	251	4	US-10-127-890-101
2	1277	100.0	251	5	US-10-717-243-101
3	1273	99.7	251	4	US-10-127-890-99
4	1273	99.7	251	5	US-10-127-890-100
5	1273	99.7	251	5	US-10-717-243-99
6	1273	99.7	251	5	US-10-717-243-100
7	1269	99.4	251	3	US-09-765-527-247
8	1269	99.4	251	4	US-10-127-890-2
9	1269	99.4	251	4	US-10-127-890-110
10	1269	99.4	251	5	US-10-717-243-2
11	1269	99.4	251	5	US-10-717-243-110
12	1269	99.4	316	4	US-10-074-596-1
13	1269	99.4	498	5	US-10-964-195-13
14	1269	99.4	507	4	US-10-074-596-11
15	1266	99.1	293	3	US-09-765-527-259
16	1266	99.1	309	3	US-09-765-527-253
17	1266	99.1	332	3	US-09-765-527-251
18	1265	99.1	751	6	US-11-084-080-26
19	1264	99.0	251	4	US-10-127-890-108
20	1264	99.0	251	5	US-10-717-243-108
21	1261	98.7	251	4	US-10-127-890-103
22	1261	98.7	251	4	US-10-127-890-104
23	1261	98.7	251	4	US-10-127-890-105
24	1261	98.7	251	4	US-10-127-890-106
25	1261	98.7	251	4	US-10-127-890-109
26	1261	98.7	251	5	US-10-717-243-103
27	1261	98.7	251	5	US-10-717-243-104

28 1261 98.7 251 5 US-10-717-243-105 Sequence 105, App
29 1261 98.7 251 5 US-10-717-243-106 Sequence 106, App
30 1261 98.7 251 5 US-10-717-243-109 Sequence 109, App
31 1260 98.7 251 4 US-10-127-890-102 Sequence 102, App
32 1260 98.7 251 4 US-10-127-890-107 Sequence 107, App
33 1260 98.7 251 4 US-10-127-890-111 Sequence 111, App
34 1260 98.7 251 5 US-10-717-243-102 Sequence 102, App
35 1260 98.7 251 5 US-10-717-243-107 Sequence 107, App
36 1260 98.7 251 5 US-10-717-243-111 Sequence 111, App
37 1212.5 94.9 513 5 US-10-926-731A-12 Sequence 12, Appl
38 1201 94.0 506 5 US-10-964-195-11 Sequence 11, Appl
39 348 27.3 263 4 US-10-127-890-4 Sequence 4, Appl
40 348 27.3 263 5 US-10-717-243-4 Sequence 4, Appl
41 346 27.1 267 4 US-10-282-935-1 Sequence 1, Appl
42 346 27.1 267 4 US-10-127-890-1 Sequence 1, Appl
43 346 27.1 267 4 US-10-440-796-1 Sequence 1, Appl
44 346 27.1 267 5 US-10-717-243-1 Sequence 1, Appl
45 346 27.1 576 4 US-10-083-336A-1 Sequence 1, Appl

ALIGNMENTS

RESULT 1

US-10-127-890-101

; Sequence 101, Application US/10127890

; Publication No. US20030166196A1

; GENERAL INFORMATION:

; APPLICANT: Better, Marc D.

; Carroll, Stephen F.

; Studnika, Gary M.

; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating

; Proteins

; NUMBER OF SEQUENCES: 173

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: McAndrews, Held & Malloy, Ltd.

; STREET: 500 West Madison Street, 34th floor

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60661

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/127,890

; FILING DATE: 23-Apr-2002

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/646,360

; FILING DATE: 13-MAY-1996

; APPLICATION NUMBER: PC7/US94/05348

; FILING DATE: 12-MAY-1994

; APPLICATION NUMBER: US 08/064,691

; FILING DATE: 12-MAY-1993

; APPLICATION NUMBER: US 07/988,430

; FILING DATE: 09-DEC-1992

; APPLICATION NUMBER: US 07/901,707

; FILING DATE: 19-JUN-1992

; APPLICATION NUMBER: US 07/787,567

; FILING DATE: 04-NOV-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: McNicholas, Janet M.

; REGISTRATION NUMBER: 32,918

; REFERENCE/DOCKET NUMBER: 200-70.P4

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 312/707-8889

; TELEFAX: 312/707-9155

; TELEX: 650 388-1248

; INFORMATION FOR SEQ ID NO: 101:

; SEQUENCE CHARACTERISTICS:

;
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 101:
US-10-127-890-101

Query Match 100.0%; Score 1277; DB 4; Length 251;
Best Local Similarity 100.0%; Pred. No. 1.2e-115; Mismatches 0; Indels 0; Gaps 0;
Matches 251; Conservative 0;

QY 1 GLDTVSFSTKGATITTYVNFNLRLVRLKPEGNHSHGIPLLRKKADDPGKAFVLVALSNDN 60
DB 1 GLDTVSFSTKGATITTYVNFNLRLVRLKPEGNHSHGIPLLRKKADDPGKAFVLVALSNDN 60

QY 61 GQLAEIAIDVTSVYVVGQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGSGYSLEGEK 120
DB 61 GQLAEIAIDVTSVYVVGQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGSGYSLEGEK 120

QY 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180

QY 181 FQQRIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
DB 181 FQQRIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240

QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 2

US-10-717-243-101
; Sequence 101, Application US/10717243
; Publication No. US20050054835A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Carroll, Stephen F.
; Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/717,243
; FILING DATE: 18-Nov-2003
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/839,765
; FILING DATE: 15-APR-1997
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:

;
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 101:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 101:
US-10-717-243-101

Query Match 100.0%; Score 1277; DB 5; Length 251;
Best Local Similarity 100.0%; Pred. No. 1.2e-115; Mismatches 0; Indels 0; Gaps 0;
Matches 251; Conservative 0;

QY 1 GLDTVSFSTKGATITTYVNFNLRLVRLKPEGNHSHGIPLLRKKADDPGKAFVLVALSNDN 60
DB 1 GLDTVSFSTKGATITTYVNFNLRLVRLKPEGNHSHGIPLLRKKADDPGKAFVLVALSNDN 60

QY 61 GQLAEIAIDVTSVYVVGQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGSGYSLEGEK 120
DB 61 GQLAEIAIDVTSVYVVGQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGSGYSLEGEK 120

QY 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180

QY 181 FQQRIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
DB 181 FQQRIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240

QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 3

US-10-127-890-99
; Sequence 99, Application US/10127890
; Publication No. US20030166196A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Carroll, Stephen F.
; Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/127,890
; FILING DATE: 23-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994

APPLICATION NUMBER: US 08/064,691
 FILING DATE: 12-MAY-1993
 APPLICATION NUMBER: US 07/988,430
 FILING DATE: 09-DEC-1992
 APPLICATION NUMBER: US 07/901,707
 FILING DATE: 19-JUN-1992
 APPLICATION NUMBER: US 07/787,567
 FILING DATE: 04-NOV-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: McNicholas, Janet M.
 REGISTRATION NUMBER: 32,918
 REFERENCE/DOCKET NUMBER: 200-70.P4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312/707-9155
 TELEX: 650 388-1248
 INFORMATION FOR SEQ ID NO: 99:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 251 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 99:

Query Match 99.7%; Score 1273; DB 4; Length 251;
 Best Local Similarity 99.6%; Pred. No. 3e-115;
 Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 GLDTSVSTKGATITVYVFNELRVKLPKGNHSHGIPLLKAKDADPGKAPVLVSLNDN 60
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Db 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETASLLVVIQMVSEAAARFTFIENQIRNN 180
Qy 181 FQOIRPANNITISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240
Db 181 FQOIRPANNITISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240
Qy 241 ALLKFVDKDPK 251
Db 241 ALLKFVDKDPK 251
  
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RESULT 4

US-10-127-890-100
 Sequence 100, Application US/10127890
 Publication No. US20030166196A1
 GENERAL INFORMATION:
 APPLICANT: Better, Marc D.
 Carroll, Stephen F.
 Studnika, Gary M.

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating Proteins

NUMBER OF SEQUENCES: 173
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: McAndrews, Held & Malloy, Ltd.
 STREET: 500 West Madison Street, 34th floor
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60661
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/127,890
 FILING DATE: 23-Apr-2002
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/646,360
 FILING DATE: 13-MAY-1996
 APPLICATION NUMBER: PCT/US94/05348
 FILING DATE: 12-MAY-1994
 APPLICATION NUMBER: US 08/064,691
 FILING DATE: 12-MAY-1993
 APPLICATION NUMBER: US 07/988,430
 FILING DATE: 09-DEC-1992
 APPLICATION NUMBER: US 07/901,707
 FILING DATE: 19-JUN-1992
 APPLICATION NUMBER: US 07/787,567
 FILING DATE: 04-NOV-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: McNicholas, Janet M.
 REGISTRATION NUMBER: 32,918
 REFERENCE/DOCKET NUMBER: 200-70.P4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312/707-8889
 TELEX: 650 388-1248
 INFORMATION FOR SEQ ID NO: 100:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 251 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 100:

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Qy 1 GLDTSVSTKGATITVYVFNELRVKLPKGNHSHGIPLLKAKDADPGKAPVLVSLNDN 60
Db 1 GLDTSVSTKGATITVYVFNELRVKLPKGNHSHGIPLLKAKDADPGKAPVLVSLNDN 60
Qy 61 GQLAEIAIDVTSVVVGQVQRNRSYFFKADPAAYEGLFKNTIKTRLHFGSGYPSLGEK 120
Db 61 GQLAEIAIDVTSVVVGQVQRNRSYFFKADPAAYEGLFKNTIKTRLHFGSGYPSLGEK 120
Qy 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETASLLVVIQMVSEAAARFTFIENQIRNN 180
Db 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETASLLVVIQMVSEAAARFTFIENQIRNN 180
Qy 181 FQOIRPANNITISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240
Db 181 FQOIRPANNITISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240
Qy 241 ALLKFVDKDPK 251
Db 241 ALLKFVDKDPK 251
  
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RESULT 5

US-10-717-243-99
 Sequence 99, Application US/10717243
 Publication No. US20050054835A1
 GENERAL INFORMATION:
 APPLICANT: Better, Marc D.
 Carroll, Stephen F.
 Studnika, Gary M.

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
 NUMBER OF SEQUENCES: 169
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: McAndrews, Held & Malloy, Ltd.
 STREET: 500 West Madison Street, 34th floor

;
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/717,243
; FILING DATE: 18-Nov-2003
; CLASSIFICATION: 530
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/839,765
; FILING DATE: 15-APR-1997
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
;
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
;
; INFORMATION FOR SEQ ID NO: 99:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 99:
US-10-717-243-99

Query Match 99.7%; Score 1273; DB 5; Length 251;
Best Local Similarity 99.6%; Pred. No. 3e-115;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLDVSFSTKGATYTYVNFNLNRVCLKPEGNHGIPLLRKADDPGKAFVLVSLNDN 60
DB 1 GLDVSFSTKGATYTYVNFNLNRVCLKPEGNHGIPLLRKADDPGKAFVLVSLNDN 60

QY 61 GOLAEIADVTSVYVVGQVNRNRSYFFKADPAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
DB 61 GOLAEIADVTSVYVVGQVNRNRSYFFKADPAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120

QY 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTETIASLLVVIQWVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTETIASLLVVIQWVSEAAARFTFIENQIRNN 180

QY 181 FQOIRPANNTISLENKWKLSFQIRTSANGMFMSEAVELERANGKYYVTVAVDQVKPKI 240
DB 181 FQOIRPANNTISLENKWKLSFQIRTSANGMFMSEAVELERANGKYYVTVAVDQVKPKI 240

QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 6
US-10-717-243-100
; Sequence 100, Application US/10717243
; Publication No. US20050054835A1
; GENERAL INFORMATION:

;
; APPLICANT: Better, Marc D.
; Carroll, Stephen P.
; Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/717,243
; FILING DATE: 18-Nov-2003
; CLASSIFICATION: 530
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/839,765
; FILING DATE: 15-APR-1997
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
;
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
;
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-10-717-243-100

Query Match 99.7%; Score 1273; DB 5; Length 251;
Best Local Similarity 99.6%; Pred. No. 3e-115;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLDVSFSTKGATYTYVNFNLNRVCLKPEGNHGIPLLRKADDPGKAFVLVSLNDN 60
DB 1 GLDVSFSTKGATYTYVNFNLNRVCLKPEGNHGIPLLRKADDPGKAFVLVSLNDN 60

QY 61 GOLAEIADVTSVYVVGQVNRNRSYFFKADPAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
DB 61 GOLAEIADVTSVYVVGQVNRNRSYFFKADPAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120

QY 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTETIASLLVVIQWVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTETIASLLVVIQWVSEAAARFTFIENQIRNN 180

QY 181 FQOIRPANNTISLENKWKLSFQIRTSANGMFMSEAVELERANGKYYVTVAVDQVKPKI 240
DB 181 FQOIRPANNTISLENKWKLSFQIRTSANGMFMSEAVELERANGKYYVTVAVDQVKPKI 240

QY 241 ALLKFVDKDPK 251

Db 241 ALLKFPVDKDPK 251

RESULT 7

US-09-765-527-247
; Sequence 247, Application US/09765527
; Patent No. US20020006638A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of Fusion Proteins and BPI-Derived Peptides
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,527
; FILING DATE: 18-Jan-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/621,803
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 247:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 247:
US-09-765-527-247

Query Match 99.4%; Score 1269; DB 3; Length 251;
Best Local Similarity 99.2%; Pred. No. 7.2e-115;
Matches 249; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 GLDVTSPSTKGATVITYVNFNLRLVKLPKGNHSHGIPLLRKKADDPGKAPVLVLSNDN 60
Db 1 GLDVTSPSTKGATVITYVNFNLRLVKLPKGNHSHGIPLLRKKADDPGKAPVLVLSNDN 60
Qy 61 GOLAEIAIDVTSVYVVGQVNRNSYFFPKADPAAYEGLFKNTIKTRLHFGGSYPSLSEGEK 120
Db 61 GOLAEIAIDVTSVYVVGQVNRNSYFFPKADPAAYEGLFKNTIKTRLHFGGSYPSLSEGEK 120
Qy 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQWVSEAAARFTFIENQIRNN 180
Db 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQWVSEAAARFTFIENQIRNN 180
Qy 181 FQQRIRPANNVTSLENKWKGLSPQIRTSANGMFSSEAVELERANGKKYVTVAVDQVVKPKI 240
Db 181 FQQRIRPANNVTSLENKWKGLSPQIRTSANGMFSSEAVELERANGKKYVTVAVDQVVKPKI 240
Qy 241 ALLKFPVDKDPK 251
Db 241 ALLKFPVDKDPK 251

RESULT 8

US-10-127-890-2
; Sequence 2, Application US/10127890
; Publication No. US20030166196A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Carroll, Stephen P.
; Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/127,890
; FILING DATE: 23-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-127-890-2

Query Match 99.4%; Score 1269; DB 4; Length 251;
Best Local Similarity 99.2%; Pred. No. 7.2e-115;
Matches 249; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 GLDVTSPSTKGATVITYVNFNLRLVKLPKGNHSHGIPLLRKKADDPGKAPVLVLSNDN 60
Db 1 GLDVTSPSTKGATVITYVNFNLRLVKLPKGNHSHGIPLLRKKADDPGKAPVLVLSNDN 60
Qy 61 GOLAEIAIDVTSVYVVGQVNRNSYFFPKADPAAYEGLFKNTIKTRLHFGGSYPSLSEGEK 120
Db 61 GOLAEIAIDVTSVYVVGQVNRNSYFFPKADPAAYEGLFKNTIKTRLHFGGSYPSLSEGEK 120
Qy 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQWVSEAAARFTFIENQIRNN 180
Db 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQWVSEAAARFTFIENQIRNN 180

US-10-717-243-2

Query Match 99.4%; Score 1269; DB 5; Length 251;
Best Local Similarity 99.2%; Pred. No. 7.2e-115;
Matches 249; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GLDTSFSTKGATITVYVNFNLRLVKLPKGNHSHGIPLLRKKADDPGKAFVLVALSNDN 60
Db |||||
Qy 1 GLDTSFSTKGATITVYVNFNLRLVKLPKGNHSHGIPLLRKKADDPGKAFVLVALSNDN 60
Db |||||

Qy 61 GOLAEIAIDVTSVVGQVVRNSYFFPKADPAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
Db 61 GOLAEIAIDVTSVVGQVVRNSYFFPKADPAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120

Qy 121 AYRETTDLGIEPLRIGIKLDENAIIDNYKPTETIASSLLVVIQMVSEARPTFIENQIRNN 180
Db 121 AYRETTDLGIEPLRIGIKLDENAIIDNYKPTETIASSLLVVIQMVSEARPTFIENQIRNN 180

Qy 181 FQORIRPANNTISLENKWKGLSPQIRTSANGMFSEAVELBRANGKYYVTVAVDQVKPKI 240
Db 181 FQORIRPANNTISLENKWKGLSPQIRTSANGMFSEAVELBRANGKYYVTVAVDQVKPKI 240

Qy 241 ALLKFVDKDPK 251
Db 241 ALLKFVDKDPK 251

RESULT 11

US-10-717-243-110
Sequence 110, Application US/10717243
Publication No. US20050054835A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
Carroll, Stephen F.
Studnicka, Gary M.

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating

Proteins

NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESS: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/717,243
FILING DATE: 18-Nov-2003
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/839,765
FILING DATE: 15-APR-1997
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889

TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPES: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 110:
US-10-717-243-110

Query Match 99.4%; Score 1269; DB 5; Length 251;
Best Local Similarity 99.6%; Pred. No. 7.2e-115;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLDTSFSTKGATITVYVNFNLRLVKLPKGNHSHGIPLLRKKADDPGKAFVLVALSNDN 60
Db 1 GLDTSFSTKGATITVYVNFNLRLVKLPKGNHSHGIPLLRKKADDPGKAFVLVALSNDN 60

Qy 61 GOLAEIAIDVTSVVGQVVRNSYFFPKADPAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
Db 61 GOLAEIAIDVTSVVGQVVRNSYFFPKADPAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120

Qy 121 AYRETTDLGIEPLRIGIKLDENAIIDNYKPTETIASSLLVVIQMVSEARPTFIENQIRNN 180
Db 121 AYRETTDLGIEPLRIGIKLDENAIIDNYKPTETIASSLLVVIQMVSEARPTFIENQIRNN 180

Qy 181 FQORIRPANNTISLENKWKGLSPQIRTSANGMFSEAVELBRANGKYYVTVAVDQVKPKI 240
Db 181 FQORIRPANNTISLENKWKGLSPQIRTSANGMFSEAVELBRANGKYYVTVAVDQVKPKI 240

Qy 241 ALLKFVDKDPK 251
Db 241 ALLKFVDKDPK 251

RESULT 12

US-10-074-596-1
Sequence 1, Application US/10074596
Publication No. US20030176331A1
GENERAL INFORMATION:
APPLICANT: ROSENBLUM, MICHAEL G.
APPLICANT: CHEUNG, LAWRENCE
TITLE OF INVENTION: MODIFIED PROTEINS, DESIGNER TOXINS, AND METHODS OF
FILE REFERENCE: CLPR-007US
CURRENT APPLICATION NUMBER: US/10/074,596
CURRENT FILING DATE: 2002-02-12
PRIOR APPLICATION NUMBER: 60/268,402
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 316
TYPE: PRT
ORGANISM: Gelonium multiflorum
US-10-074-596-1

Query Match 99.4%; Score 1269; DB 4; Length 316;
Best Local Similarity 99.2%; Pred. No. 1e-114;
Matches 249; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GLDTSFSTKGATITVYVNFNLRLVKLPKGNHSHGIPLLRKKADDPGKAFVLVALSNDN 60
Db 47 GLDTSFSTKGATITVYVNFNLRLVKLPKGNHSHGIPLLRKKADDPGKAFVLVALSNDN 106

Qy 61 GOLAEIAIDVTSVVGQVVRNSYFFPKADPAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
Db 107 GOLAEIAIDVTSVVGQVVRNSYFFPKADPAAYEGLFKNTIKTRLHFGGSYPSLEGEK 166

Qy 121 AYRETTDLGIEPLRIGIKLDENAIIDNYKPTETIASSLLVVIQMVSEARPTFIENQIRNN 180
Db 167 AYRETTDLGIEPLRIGIKLDENAIIDNYKPTETIASSLLVVIQMVSEARPTFIENQIRNN 226


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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 259:
US-09-765-527-259

Query Match          99.1%; Score 1266; DB 3; Length 293;
Best Local Similarity 98.8%; Pred. No. 1.8e-114;
Matches 248; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GLDTVSPSTKGATITVYNFLNELRVKLPKGNHGIPLLRKKADDPKAPVLVALSNDN 60
Db 23 GLDTVSPSTKGATITVYNFLNELRVKLPKGNHGIPLLRKKADDPKAPVLVALSNDN 82
QY 61 GOLAEIAIDVTSVYVVGQVNRNRYFFPKADPAAYEGLFKNTIKTRLHFGSGYPSLEGEK 120
Db 83 GOLAEIAIDVTSVYVVGQVNRNRYFFPKADPAAYEGLFKNTIKTRLHFGSGYPSLEGEK 142
QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLIVVQMVSEAAARFTFIENQIRNN 180
Db 143 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLIVVQMVSEAAARFTFIENQIRNN 202
QY 181 FQQRIRPANNTISLENKWKLSFOIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240
Db 203 FQQRIRPANNTISLENKWKLSFOIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 262
QY 241 ALLKRFVDKDPK 251
Db 263 ALLKRFVDKDPK 273
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Search completed: February 10, 2006, 10:44:48
Job time : 164.937 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 10, 2006, 10:39:04 ; Search time 12.9668 Seconds
(without alignments)
254.015 Million cell updates/sec

Title: US-10-717-243-101

Perfect score: 1277

Sequence: 1 GLDTVSFSTKGATYITVNF.....AVDQVKFKIALKXVDKDPK 251

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 97014 seqs, 13122538 residues

Total number of hits satisfying chosen parameters: 97014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:

- 1: /cgm2_6/ptodata/1/pubppaa/US08_NEW_PUB.pdb:
- 2: /cgm2_6/ptodata/1/pubppaa/US06_NEW_PUB.pdb:
- 3: /cgm2_6/ptodata/1/pubppaa/US07_NEW_PUB.pdb:
- 4: /cgm2_6/ptodata/1/pubppaa/US09_NEW_PUB.pdb:
- 5: /cgm2_6/ptodata/1/pubppaa/US05_NEW_PUB.pdb:
- 6: /cgm2_6/ptodata/1/pubppaa/US10_NEW_PUB.pdb:
- 7: /cgm2_6/ptodata/1/pubppaa/US11_NEW_PUB.pdb:
- 8: /cgm2_6/ptodata/1/pubppaa/US60_NEW_PUB.pdb:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	346	27.1	268	7	US-11-010-795-24
2	346	27.1	576	6	US-10-923-022-1
3	346	27.1	630	6	US-10-893-584-274
4	327	25.6	313	7	US-11-010-795-20
5	307	24.0	267	6	US-10-517-707A-1
6	248.5	19.5	200	6	US-10-923-022-10
7	246.5	19.3	190	6	US-10-923-022-11
8	245.5	19.2	198	6	US-10-923-022-3
9	245.5	19.2	198	6	US-10-923-022-7
10	245.5	19.2	199	6	US-10-923-022-5
11	243.5	19.1	188	6	US-10-923-022-4
12	243.5	19.1	188	6	US-10-923-022-8
13	243.5	19.1	189	6	US-10-923-022-6
14	240	18.8	267	6	US-10-517-707A-7
15	239	18.7	185	6	US-10-923-022-9
16	204	16.0	310	7	US-11-010-795-22
17	176.5	13.8	179	6	US-10-923-022-2
18	85.5	6.7	315	7	US-11-010-795-28
19	83	6.5	319	7	US-11-010-795-26
20	80.5	6.3	386	7	US-11-022-562-229
21	80.5	6.3	365	7	US-11-102-978-9
22	80.5	6.3	365	7	US-11-080-991-78
23	80.5	6.3	1088	7	US-11-098-686-10718
24	80	6.3	377	6	US-10-793-626-3014
25	80	6.3	459	6	US-10-453-372-1044

26	79	6.2	934	7	US-11-188-743-19	Sequence 19, Appl
27	79	6.2	934	7	US-11-183-294-20	Sequence 20, Appl
28	78.5	6.1	303	7	US-11-156-084-232	Sequence 232, App
29	78	6.1	951	6	US-10-453-372-1012	Sequence 1012, App
30	77.5	6.1	483	7	US-11-052-554A-107	Sequence 107, App
31	77	6.0	459	6	US-10-453-372-1018	Sequence 1018, App
32	77	6.0	459	6	US-10-453-372-1046	Sequence 1046, App
33	77	6.0	459	6	US-10-453-372-1048	Sequence 1048, App
34	77	6.0	459	6	US-10-453-372-1050	Sequence 1050, App
35	77	6.0	475	6	US-10-793-626-2076	Sequence 2076, App
36	77	6.0	627	6	US-10-873-528-191	Sequence 191, App
37	77	6.0	719	6	US-10-793-626-1548	Sequence 1548, App
38	77	6.0	947	6	US-10-453-372-1010	Sequence 1010, App
39	77	6.0	962	6	US-10-453-372-1042	Sequence 1042, App
40	76.5	6.0	417	6	US-10-995-561-791	Sequence 791, App
41	76.5	6.0	417	7	US-11-110-851-61	Sequence 61, Appl
42	75.5	5.9	1183	7	US-11-115-639-13	Sequence 13, Appl
43	75.5	5.9	1183	7	US-11-115-639-14	Sequence 14, Appl
44	75.5	5.9	1183	7	US-11-115-639-15	Sequence 15, Appl
45	75.5	5.9	1183	7	US-11-115-639-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1

US-11-010-795-24
; Sequence 24, Application US/11010795
; Publication No. US20060005271A1
; GENERAL INFORMATION:
; APPLICANT: TUNER, NILGUN E.
; TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING L3 DELTA PROTEINS ARE
; TITLE OF INVENTION: RESISTANT TO TRICHOECENE FUNGAL TOXINS
; FILE REFERENCE: OCIRS 3.0-085
; CURRENT APPLICATION NUMBER: US/11/010,795
; PRIOR FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: 60/529,348
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 24
; TYPE: PRT
; ORGANISM: Ricinus communis
US-11-010-795-24

Query Match	27.1%	Score 346;	DB 7;	Length 268;
Best Local Similarity	36.8%	Pred. No. 1e-24;		
Matches	93;	Conservative 45;	Mismatches 99;	Indels 16; Gaps 9;
Qy	5	VSFSTKGATVITVYVNFLELRLVKLKPEGN-SHGIPILLRKKADDP-GKAFVLVALSDNGQ	62	
Db	10	INFTTAGATVQSTVFIRAVRGRLTTGADVHRHIVLPNVRGLPQRFILVELSNHAE	69	
Qy	63	LABIAIDVTSVYVYVGVQVNRNRSYFFKADP-----AAVEGLFKNTIKTR--LHFGGSYPS	115	
Db	70	SVTLALDVNAYVGVYRAGNSAYFFH--PDNQDEAETHLFTD-VQNRVTFAGGNYDR	126	
Qy	116	LEGEKA-YRETTDLGIEPIRIGIKLDENADINYPTEIASLLWVQMVSEARFTFIE	174	
Db	127	LEQLAGLNRENIEELNGPLEEALISALVYVSTGGTQLPTLARSPIICIMISEARFOYIE	186	
Qy	175	NQIRN--NFQIRRPANNTISLENKVKLSFQRTSGANGMFSEAVLERANGKYYVTA	232	
Db	187	GENKTRIRYRRSAPDPSPVITLNSWGLRSLTAIQESN-QGAFASPIQLORRNGSKFSYD	245	
Qy	233	VDOVKPKIALKX	245	
Db	246	VSILIPILALMVY	258	

RESULT 2


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; LENGTH: 630
; TYPE: PRT
; ORGANISM: Artificial Sequence

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; OTHER INFORMATION: Xaa=Thr, Ser
; OTHER INFORMATION: Xaa=Pro
; OTHER INFORMATION: Xaa=Ala, Gly, Pro
; OTHER INFORMATION: Xaa=Ala, Gly, Pro
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 94, 95, 114
; OTHER INFORMATION: Xaa=Ala, Gly, Pro, His, Asp, Glu, Asn, Gln, Lys,
; OTHER INFORMATION: Arg, Ser, Thr
; OTHER INFORMATION: Xaa=Ala, Gly, Pro
; OTHER INFORMATION: Xaa=Ala, Gly, Pro
; OTHER INFORMATION: Xaa=Ala, Gly, Pro
; OTHER INFORMATION: Xaa=Ala, Pro, Ser, Thr, His, Lys
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 117, 119, 120, 121
; OTHER INFORMATION: Xaa=Thr
; OTHER INFORMATION: Xaa=His
; OTHER INFORMATION: Xaa=Ser
; OTHER INFORMATION: Xaa=Ala, Ser, thr, Pro, Asn, Asp, Glu, Gly, His,
; OTHER INFORMATION: Lys, Gln
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 122, 125, 139, 132
; OTHER INFORMATION: Xaa=Thr
; OTHER INFORMATION: Xaa=Ala, Pro
; OTHER INFORMATION: Xaa=Ala, Ile, Phe, Gly, Met, Pro, Val, Trp, Tyr
; OTHER INFORMATION: Xaa=Phe, Pro, Trp
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (137) ... (143)
; OTHER INFORMATION: Xaa=Ala, Gly, Pro
; OTHER INFORMATION: Xaa=Ala, Gly, Pro
; OTHER INFORMATION: Xaa=Ala, Gly, Pro
; OTHER INFORMATION: Xaa=Ala, Gly, Pro
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (152) ... (155)
; OTHER INFORMATION: Xaa=Ala, Gly, Pro, Ser, Thr
; OTHER INFORMATION: Xaa=Ala, Gly, Pro, Ile, Met, Ser, Thr
; OTHER INFORMATION: Xaa=Ala, Gly, Pro
; OTHER INFORMATION: Xaa=Ala, Gly, Pro, Ser, Thr, His, Asp, Asn, Gln,
; OTHER INFORMATION: Lys, Arg
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (187) ... (198)
; OTHER INFORMATION: Xaa=Ala, Gly, Pro, Thr, Ser, His, Lys, Arg, Asp,
; OTHER INFORMATION: Glu, Asn, Gln
; OTHER INFORMATION: Xaa=Ala, Gly, Pro, Thr, Ser, His, Lys, Arg, Asp,
; OTHER INFORMATION: Glu, Asn, Gln
; OTHER INFORMATION: Xaa=Gln
; OTHER INFORMATION: Xaa=His, Lys, Arg, Asp, Glu, Asn,, Phe, Leu, Pro,
; OTHER INFORMATION: Ser, Tyr, Trp
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (200) ... (202)
; OTHER INFORMATION: Xaa=Ala, Gly, Pro, Thr, Ser, His, Lys, Arg, Asp,
; OTHER INFORMATION: Glu, Asn, Gln
; OTHER INFORMATION: Xaa=Asp
US-10-517-707A-7

Query Match 18.8%; Score 240; DB 6; Length 267;
Best Local Similarity 30.5%; Pred. No. 5.9e-15;
Matches 75; Conservative 33; Mismatches 124; Indels 14; Gaps 7;

Qy 5 VSFSTKGATYTYVNFNLRLVKLPKGNHGIPLLRKADDPGKAFVLVALSNDNGOLA 64
Db 2 VSFRLSGATTSTGYGFIKRLREALPYERKVNIPILRRSSIGSGR-YKKLXLTXXADETX 60

Qy 65 EIAIDVTSVYVGVQVNRNSYFFKDA-PDAAYEGLEPKWT-IKTRLHFGGSYPSLEGEKAY 122
Db 61 SVAXDXTNVYTMGLAGDVSYFFNEASATEAAKXFKDAKKKXLTLPYSGNY-----ERX 114

Qy 123 RETTDLGIEPLRIGIKLDENAIIDNYKPT--EIASLLVVIQMVSEAAARFTFIENQIRNN 180

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Db 115 QTXAXXXENKXPLGXPAIXSAXTXXYXTASSAASAXXXIXQTAESARYKFIQQIGKR 174
Qy 181 FQORIRPANNITISLENKWKLSFOIRTSGA-NGMFPSEAVLERANGKKYVVT--AVDOVK 237
Db 175 VDKTFLPSLATXSKENNWSAXSQXQXASTNNGQFSPVVLIDGNNQORSITNASARVVT 234
Qy 238 PKIALL 243
Db 235 SNIALL 240

RESULT 15
US-10-923-022-9
; Sequence 9, Application US/10923022
; Publication No. US20060009619A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Byrnie, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452USO (RiID 01-58)
; CURRENT APPLICATION NUMBER: US/10/923,022
; CURRENT FILING DATE: 2004-08-23
; PRIOR APPLICATION NUMBER: US/10/083,336
; PRIOR FILING DATE: 2002-02-27
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-923-022-9

Query Match 18.7%; Score 239; DB 6; Length 185;
Best Local Similarity 36.3%; Pred. No. 4.4e-15;
Matches 69; Conservative 30; Mismatches 65; Indels 26; Gaps 8;

Qy 5 VSFSTKGATYTYVNFNLRLVKLPKGNHGIPLLRKADDPGKAFVLVALSNDNGOLA 64
Db 9 INFRTAGATVQSYTNFIRAVRGRLT---NRVGLPI-----NQRFILVELSNHAEISV 57

Qy 65 EIAIDVTSVYVGVQVNRNSYFFKDA-PD-----AAYEGLEPKNTIKTR--LHFGGSYPSLE 117
Db 58 TLALDVTNAYVGVYRAGNSAYFFH--PDNQEDAEATHLFTD-VQNRYYTAFAGNYDRLE 114

Qy 118 GERA-YRETTDLGIEPLRIGIKLDENAIIDNYKPTFIASSLLVVIQMVSEAAARFTFIENQ 176
Db 115 QLAGNLRNIELGNGLPEEAISALYYYSTGTGTQTLPLARSFIICIQMISEAARFQYIEGE 174

Qy 177 IRNPFQORIR 186
Db 175 MRT----RIR 180

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Search completed: February 10, 2006, 10:45:21
Job time : 13.9668 secs